

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2003, 01:44:12 ; Search time 123 Seconds
(without alignments)

3050.209 Million cell updates/sec

Title: US-09-904-389-2

Perfect score: 4435

Sequence: 1 MEMPGRRSDYLLSQIPDEE.....KPMTKQAPQOQRDTLSVM 850

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Xgapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US0904389/runat_23102003_171709_45/app_query.fasta_1.1031
-DB=issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORMEXT=HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0904389@cgn_1_1_56@runat_23102003_171709_45 -NCPU=6 -ICPU=3
-NO.WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2742.5	61.8	2890	1	US-07-928-464-1 Sequence 1, Appli
2	2742.5	61.8	2890	5	PCT-US93-07347-1 Sequence 1, Appli
3	2742.5	61.8	3033	1	US-08-003-311B-1 Sequence 1, Appli
4	2742.5	61.8	3033	1	US-08-261-432-1 Sequence 3, Appli
5	2072	46.7	5890	1	US-07-928-464-3 Sequence 3, Appli
6	2072	46.7	5890	5	PCT-US93-07347-3 Sequence 3, Appli
7	2072	46.7	6312	1	US-08-003-311B-3 Sequence 3, Appli
8	2072	46.7	6312	1	US-08-261-432-3 Sequence 3, Appli
9	2069	46.7	6312	1	US-08-003-311B-7 Sequence 7, Appli
10	2069	46.7	6312	1	US-08-261-432-7 Sequence 7, Appli
11	2068	46.6	5890	1	US-07-928-464-6 Sequence 6, Appli
12	2068	46.6	5890	5	PCT-US93-07347-6 Sequence 6, Appli

13	2068	46.6	6312	1	US-08-003-311B-6 Sequence 6, Appli
14	2068	46.6	6312	1	US-08-261-432-6 Sequence 6, Appli
15	2063	46.5	5890	1	US-07-928-464-5 Sequence 5, Appli
16	2063	46.5	5890	5	PCT-US93-07347-5 Sequence 5, Appli
17	2063	46.5	6312	1	US-08-003-311B-5 Sequence 5, Appli
18	2063	46.5	6312	1	US-08-261-432-5 Sequence 5, Appli
19	2024	45.6	5873	1	US-07-928-464-4 Sequence 4, Appli
20	2024	45.6	5873	5	PCT-US93-07347-4 Sequence 4, Appli
21	2024	45.6	6295	1	US-08-003-311B-4 Sequence 4, Appli
22	2024	45.6	6295	1	US-08-261-432-4 Sequence 4, Appli
23	507	11.4	2119	4	US-09-399-588-1 Sequence 1, Appli
24	504.5	11.4	1365	3	US-09-221-235-6 Sequence 6, Appli
25	504.5	11.4	1365	3	US-09-221-235-6 Sequence 6, Appli
26	504.5	11.4	1365	3	US-09-221-236-6 Sequence 6, Appli
27	504.5	11.4	1365	3	US-09-221-236-6 Sequence 6, Appli
28	504.5	11.4	1365	3	US-09-221-416-6 Sequence 6, Appli
29	504.5	11.4	1365	3	US-09-221-416-6 Sequence 6, Appli
30	504.5	11.4	1365	3	US-09-163-115-6 Sequence 6, Appli
31	504.5	11.4	1365	3	US-09-221-528-6 Sequence 6, Appli
32	504.5	11.4	1365	3	US-09-593-553-6 Sequence 6, Appli
33	504.5	11.4	1365	3	US-09-221-237-6 Sequence 6, Appli
34	504.5	11.4	2120	3	US-09-221-235-4 Sequence 4, Appli
35	504.5	11.4	2120	3	US-09-221-235-4 Sequence 4, Appli
36	504.5	11.4	2120	3	US-09-221-527-4 Sequence 4, Appli
37	504.5	11.4	2120	3	US-09-221-236-4 Sequence 4, Appli
38	504.5	11.4	2120	3	US-09-221-416-4 Sequence 4, Appli
39	504.5	11.4	2120	3	US-09-221-245-4 Sequence 4, Appli
40	504.5	11.4	2120	3	US-09-163-115-4 Sequence 4, Appli
41	504.5	11.4	2120	3	US-09-221-528-4 Sequence 4, Appli
42	504.5	11.4	2120	3	US-09-593-553-4 Sequence 4, Appli
43	504.5	11.4	2120	3	US-09-221-237-4 Sequence 4, Appli
44	469.5	10.6	2510	2	US-08-888-982A-42 Sequence 42, Appli
45	469.5	10.6	2510	4	US-09-462-261-42 Sequence 42, Appli

ALIGNMENTS

RESULT 1
US-07-928-464-1
; Sequence 1, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2890 base pairs

TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 118..2583
 US-07-928-464-1

Alignment Scores:

Pred. No.: 2,82e-272 Length: 2890
 Score: 2742.50 Matches: 546
 Percent Similarity: 73.63% Conservative: 99
 Best Local Similarity: 62.33% Mismatches: 144
 Query Match: 61.84% Indels: 87
 DB: 1 Gaps: 14

US-09-904-389-2 (1-850) x US-07-928-464-1 (1-2890)

QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
 DB 118 ATGGAAATGCCGGTAGAAGACTTAATACACITTCCTTAGTCAATTTCTCAGCATCAG 177
 QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
 DB 178 GTGTCAAGTTCCGTCACCGGAGCTCCTCCGCTCCTCCTATATGTTCTCGAGCGAAAC 237
 QY 36 -----GlyGlyAsnValIleLeuGlyArgThrAspArg---ValPheAsp 49
 DB 238 AGGAGCAACCATACACGGCGGACACCGGAAAGCTAAGCGGAGAGAGCGGATTGAT 297
 QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
 DB 298 TGGGATCCTAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 357
 QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
 DB 358 GGGAAATAATATGTAATGCTTCTCTAGGGTTGCAAGGCAATCCAGTGGAGTAGTTTC 417
 QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
 DB 418 GGTGAGAGCTCTTGTCTCTGGGGAATATTACATGCTACGCTTCT---GGCGCGCTAAC 474
 QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
 DB 475 GAGATCGAATCTGTGGATTCTCTCAAGATGATGGGTTTAGGCTTGGATTGTGTGTGT 534
 QY 119 -----MethLeuAlaValGlySerGlyGly---SerSerGlyGly 130
 DB 535 CGAGGAGATTGAGGATACAGATGGCGCGGACTCCGCTGGAGGGTCTTCATCTGGGAAG 594
 QY 131 SerTrpAlaGlnInThrGluSerPheGlnLeuGlnInProLeuValLeuArgLeu 150
 DB 595 AGCTGGGCGCAGCAGCGGAGAGATTATCAGCTGGAGCTTGCATTTAGGCTTTAAGGCTT 654
 QY 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
 DB 655 TCGTCGAGGCTACTGTGTGGCAGCATCCGAACCTTCTGGATCTGTACCGGACGAGTCT 714
 QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190
 DB 715 GCTTTACGGACTCGCCAAAGTTTCACCCGAAACCGGTTTTCATCTGTTCTGGTTTATGCG 774
 QY 191 CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro 210
 DB 775 TCGTTATCTACTATGATAAAGTCTCTGATGGTTTATATGATGATGATGATGATGATGCC 834
 QY 211 TyrValTrpSerLeuCysThrAsnLeuGlnAspGlyArgIleProSerPheGluSer 230
 DB 835 TATATTGGACCTTATGTCATCGACCTGATGAAGTGTGCGATCCCTTCAATTGAATCA 894
 QY 231 LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis 250

DB 895 TTAAGAGCTGTTGATTCTGTGTTGATTCTTCGCTTGAAGCGATCATAGTTGATAGCGGT 954
 QY 251 SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysVal 270
 DB 955 AGTGATCCAGCTTCCAGAACTTCAATAGATGCCAGCATATCTTGTAGTCGATT 1014
 QY 271 ThrThrLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySer 290
 DB 1015 ACCACAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTATGGGGGGTCCA 1074
 QY 291 ValSerGluGlyGluAspAspLeuValSerAlaTrpLysGluCysSerAspAspLeuLys 310
 DB 1075 GTTATCATGGGGGAAGATGAGTTGTTCCCATGTGGAGAGAGTGCATGTGTCATAAAA 1134
 QY 311 GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis 330
 DB 1135 GAA---ATCTTTAAAGTGTGGTTCCTCCATAGTAGCTCTCTGTGGACTCTGAGACAT 1191
 QY 331 ArgAlaLeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys 350
 DB 1192 CGAGCTTTTACTCTTCAAGTACTGGCTGACATAATTGATTTTACCCTGTGCAATGGCCAAA 1251
 QY 351 GlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPheGlyLeuAsp 370
 DB 1252 GGATGTAATATTGTAATAGACAGCATGCCGCTTCGCTGTGTGAGTTTGGGCTTGAT 1311
 QY 371 ArgGluTyrIleLeuAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeu 390
 DB 1312 AGGAGTACTCGTGGTATTAGTGAAGACGAGTCACTTATGGGAGCCCTGATTCCTTG 1371
 QY 391 LeuAsnGlyProSerSerIleSerSerProLeuArgPheProArgLeuLysPro 410
 DB 1372 CTAAATGCTTCCTTCATCTCATCTCAATTTCTCTCTCGGTTTCCACGACCAAGGCA 1431
 QY 411 IleGluSerThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSer 430
 DB 1432 GTTGAACCCGCGAGTCGATTAGTGTACTAGCAACAATATTTCTCCGATAGCCGCTCT 1491
 QY 431 LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla 450
 DB 1492 CTAAATCTGTTTTCATCTCTCATCAGAT-----CATATGGGA 1530
 QY 451 PheSerValTyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal 470
 DB 1531 TTCTCAATGTTTCATAGCAATATGATAATCCGGTGGAGAGAAATGACGCTATGGCAGAA 1590
 QY 471 ThrGlyAspLysAspArgAsnSerGlnLeuLeuAsnLysAlaAlaGlnLeuAsnThr 490
 DB 1591 AATGGTGGT----- 1599
 QY 491 GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
 DB 1600 -----GGGTCT 1605
 QY 511 ThrProPheValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAsp 530
 DB 1606 TTGCCACCCAGTGTATATGCTTCA----- 1632
 QY 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe 550
 DB 1633 ---CAGAACATGATGCGTGGCTCAAAATCAAAATGAAGACAGCACCTATGAATGCCACCA 1689
 QY 551 ValHisGlySerGlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeu 570
 DB 1690 ATCATGACCGAGTTCCAAACAGGGCAATAGGAACTTGGAACTTGGATGGTGGATGATG 1749
 QY 571 ValIleProTyrThrAspLeuAspLeuArgGlyLysIleGlyAlaGlySerPheGlyThr 590
 DB 1750 GACATCCCGTGTGTGATCTTAATAAAGAAAGAAAGATTGGAGCAGGTTCTCTTGGCACT 1809
 QY 591 ValTyrArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThrGluGlnAsp 610
 DB 1810 GTCCACCGTGTGAGTGGCATGGCTCGATGTTGCTGTGAAATTTCTCATGGAGCAAGAC 1869

QY 611 PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg 630
Db 1870 TTCATGCTGAGCGTGTAAATAGTCTTAAAGAGGTTGCATAATGAAACGCTTCGC 1929
QY 631 HisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeuSerIleVal 650
Db 1930 CACCTTAAATGTTCTCTCATGGTGGCGGCATCTCAACCTCCAAATTTGCAATAGT 1989
QY 651 ThrGluTyrSerArgLysSerLeuValHisLysSerGlyValLysAsp 670
Db 1990 ACAGATAATTTGCAAGAGTATTTATACAGCTTTTGCATAAAAGTGGACGAGGAG 2049
QY 671 ---IleAsnGluThrArgGluLeuMetAlaPheAspValAlaLysGlyMetAsnTyr 689
Db 2050 CAATTAGATGAGAGAGCTCCCTGAGTATGGCTTATGATGTGCTTAAGGAATGAATAT 2109
QY 690 LeuHisArgAspProProIleValHisArgAspLeuLysSerProAsnLeuVal 709
Db 2110 CTTCAATGCGCAATCCTCAATTTGTCATAGATCTAAATCTCCAACTTATTTGGT 2169
QY 710 AspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThr 729
Db 2170 GACAAAAATATACAGTCAAGTTTGTGATTTGTCTCTCGGATTAAGGCCAGCAGC 2229
QY 730 PheLeuSerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluValLeuArg 749
Db 2230 TTTCTTTCTCGAAGTCAGCAGCTGGAACCCCGAGTGGATGGACCAAGAGTCTGGGA 2289
QY 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrGluLeu 769
Db 2290 GATGAGCCCTTAATGAAAGTCAGATGTGTACAGCTTCGGGGTCATCTTGTGGAGCTT 2349
QY 770 AlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValValAlaAlaValGly 789
Db 2350 GCTAGATTCGACCAACCATGGGTAACTTAATCCGGCTCAGTTGTAGCTGCGTGGT 2409
QY 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle 809
Db 2410 TTCAGTGTAAACGGCTGAGATCCCGGTAAATCTGAAATCTCAGTTGCAAGCCATAATC 2469
QY 810 ValAlaCysTyrAlaAspGluProTyrLysArgProSerPheSerSerIleMetGluThr 829
Db 2470 GAGGTGTGTGGACCAATGAGCAATGGAAGCTCATTTGCACTATATGAGACTTG 2529
QY 830 LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp 845
Db 2530 CTAAGACCAATGATCAATCAGCGGTCTCTCCGCCCAACCGCTCGAT 2577

RESULT 2

PCT-US93-07347-1
; Sequence 1, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347

; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
; PCT-US93-07347-1

Alignment Scores:
Pred. No.: 2,82e-272 Length: 2890
Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: 5 Gaps: 14

US-09-904-389-2 (1-850) x PCT-US93-07347-1 (1-2890)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 118 ATGGAATGCCGGTAGAAGATCTAATACACTTGTCTTGTCAATTTCTGACGATCAG 177
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 178 GTGCAGTTTCGTCACCGAGCTCCTCCGCTCCTATGATCTTGTGCGAGAAAC 237
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 238 AGGACCAACCATACAGCGGGAACACCGGGAAGCTAAGCGGAGAGAGCGGATTTGAT 297
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 298 TGGGATCTCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 357
QY 66 Gly-----AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 358 GGAATAATATGATGCTTCGTCCTAGGCTTGCAGAAAGCAATCCAGTGGAGTAGTTTC 417
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 418 GGTGAGAGCTCTTGTCTGGGGATTTATATACATGCTACGCTTTCT---GCGGCGGCTAAC 474
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
Db 475 GAGATCGAATCTGTGGATTTCTCCTCAGATGATGGT---TAGGCTTGGATTGGTGGT 534
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 535 GGAGGAGATTGAGGATACAGATCGCGCGGAGCTCCGCTGGAGGCTTCTCATCTGGGAAG 594
QY 131 SerTrpAlaGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 595 AGCTGGGCGCAGCAGCAGGAGAGATTAATCAGCTGCGCTTGCATTGGGCTTAAGGCTT 654
QY 151 SerSerAsp***ThrCysAlaAspProAsnPheMetAspProIleProAspGluAla 170
Db 655 TCGTCGGAGGCTACTTGTGCGGAGATCCGAACCTTCTGGATCTCTGTACCGGAGATCT 714
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190
Db 715 GCTTTACGAGACTTCGCCAAGTTTCAGCCGAAACCGTTTTCATCATCTTTCTGGGTTAATGGC 774

QY	191	CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro	210
DB	775	GCCTATCGTACTATGATAAAGTTCCTGATGGGTATTATATGATGAATGGTCTGGATCCC	834
QY	211	TyrValTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer	230
DB	835	TATATTGGACCTTATGCATCGACCTGCATGAAGTGTGCGATCCCTTCATTTGAATCA	894
QY	231	LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis	250
DB	895	TTAAGAGCTGTTGATTCTGGTGTGATTCTTCGCTTGAGCGCATCATAGTTGATAGCGGT	954
QY	251	SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysVal	270
DB	955	AGTGATCAGCGCTTCAGGAACCTTCACATAGATGATCCAGCATATCTTTAGTGGCAT	1014
QY	271	ThrThrLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySer	290
DB	1015	ACCACAAAGAGGTGTTGATCAGCTGGCAAGCTTATCTGCAATGTATCGGGGGTCCA	1074
QY	291	ValSerGluGlyGluAspAspLeuValSerAlaIleLysGluCysSerAspAspLeuLys	310
DB	1075	GTTATCATCGGGGAAGATGAGTTGGTTCCTGCTGGAGAGTGCATTGATGGCTTAAA	1134
QY	311	GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis	330
DB	1135	GAA---ATCTTTAAAGTGGTGGTTCCTATAGTAGTAGGCTCTCTGTTGGACTCTGCAGACAT	1191
QY	331	ArgAlaLeuLeuPheLeuValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys	350
DB	1192	CGAGCTTTTACTCTTCAAGTACTGGCTGCATTAATTGATTTTACCCTGTGCAATTGCCAAA	1251
QY	351	GlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPheGlyLeuAsp	370
DB	1252	GGATGTAATATTGTAATAGACAGCATCGCGCTTCGTGCTTGTTCAGGTTTGGGCTTGAT	1311
QY	371	ArgGluTyrLeuIleAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeu	390
DB	1312	AGGGAGTACCTGGTTGATTAGTAGGAAGCCAGGTCACTTATGGGAGCTGATTCCTTG	1371
QY	391	LeuAsnGlyProSerSerIleSerIleSerSerProLeuArgPheProArgLeuLysPro	410
DB	1372	CTAAATGTGCTCTTATCTATCTCAATTTCTTCCTCTCGGTTTCCACGACCAAGGCCA	1431
QY	411	IleGluSerThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSer	430
DB	1432	GTTGAACCGCAGTCGATTTTAGGTACTAGCCAAACAATAATTCTCCGATAGCCAGTCT	1491
QY	431	LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla	450
DB	1492	CTTAATCTTGTTTCGATCTCGCATCAGAT-----GATATGGGA	1530
QY	451	PheSerValTyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal	470
DB	1531	TTCTCAATGTTTCATAGGCAATATGATAATCCGGTGGAGAGATGACGCATTTGCCAAA	1590
QY	471	ThrGlyAspLysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThr	490
DB	1591	AATGGTGGT-----	1599
QY	491	GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer	510
DB	1600	-----GGGTCT	1605
QY	511	ThrProPheValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAsp	530
DB	1606	TTGCCACCCAGTGTAAATATGCTTCCA-----	1632
QY	531	SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe	550
DB	1633	---CAGAACATGATCGTGCCTCAAAATTCAAATTCGAGACGACCTATGATGATGCCCCACA	1689

RESULT 3

RESULTS
US-08-003-311B-1

US-08-003-311B-1
; Sequence 1, Application US/08003311B

; Patent No. 5444166

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J

TITLE OF INVENTION: Constitutive Triple Response Gene

TITLE OF INVENTION: and Mutations

; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and

ADDRESSEE: No. 5444166ris

Qy	551	ValHisGlySerGlnLeuLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeu	570
Db	1690	ATCAGTCAGCCAGTTCMAACACGGCGCAATATGAGCAACTGGACCTTGATGGTGATGAT	1749
Qy	571	ValIleProTrpThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThr	590
Db	1750	GACATCCCGTGTGTGATCTTAATAATAAAGAAAAAGATTGGACAGAGTCTCTTTGGCACT	1809
Qy	591	ValTyArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThrGluGlnAsp	610
Db	1810	GTCCACCGTGTGAGTGGCATGCTCGGATGTCTGTGMAAATTCTCATGGACAGAC	1869
Qy	611	PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg	630
Db	1870	TTCCATGCTGAGCGTGTATATAGTGTCTTAAGAGAGTTCGATTAATCAACAGCGCTTCGC	1929
Qy	631	HisProAsnIleValLeuPheMetGlyAlaValThrLysProAsnLeuSerIleVal	650
Db	1930	CACCCATACTGTGTCTTCATCGGTGGGTCTCACTCAACCTCCAAATTTGTCATATGTG	1989
Qy	651	ThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAsp	670
Db	1990	ACAGAAATATTGTCACAGAGTAGTTTATACAGACTTTTGCATAAAGATGGAGCAAGGAG	2049
Qy	671	---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr	689
Db	2050	CAATTAGATGAGACGTCGCCGTGAGTAGTGGCTTATGATGTGGCTAAGGGAATGAATTAT	2109
Qy	690	LeuHisArgArgProProIleValHisArgAspLeuLysSerProAsnLeuLeuVal	709
Db	2110	CTTCACAATCGCAATCTCCAAATGTGTCATAGAGATCTAAATCTCCAAACTTATTGGTT	2169
Qy	710	AspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThr	729
Db	2170	GACAAAAAATATACAGTCNAGTTTGTGATTTGGTCTCTCCGGATTGAAGCCAGCAGC	2229
Qy	730	PheLeuSerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluValLeuArg	749
Db	2230	TTTCTTCTCGAAGTCAGACGTGGAAACCCCGAGTGGATGGCACCAAGATCTCGCGA	2289
Qy	750	AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTrpGluLeu	769
Db	2290	GATGAGCCGTCTAATGAAAAGTCAGATGTGTACAGCTTCGGGGTCACTCTGTGGGAGCTT	2349
Qy	770	AlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnValValAlaAlaValGly	789
Db	2350	GCTACATTGCAACCAACCATGGGGTAACTTAATCCGGCTCAGGTTGAGCTCGGCTTGGT	2409
Qy	790	PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle	809
Db	2410	TTCAAGTGTAAACGGCTGGAGATCCCGCGTAATCTGAATCTCTCAGGTCGACCCATAATC	2469
Qy	810	ValAlaCysTrpAlaAspGluProTrpLysArgProSerPheSerSerIleMetGluThr	829
Db	2470	GAGGGTGTGTGACCAATGAGCCATGGAGCGTCCATCATTTTGCAACTATATATGCACTTG	2529
Qy	830	LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp	845
Db	2530	CTAAGACATTGATCAATATCAGCGTTCTCTCCGCCCAACCGCTCGGAT	2577

RESULT 3

RESULTS
US-08-003-311B-1

US-08-003-311B-1
; Sequence 1, Application US/08003311B

; Patent No. 5444166

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J

TITLE OF INVENTION: Constitutive Triple Response Gene

TITLE OF INVENTION: and Mutations

; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and

ADDRESSEE: No. 5444166ris

STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/003.311B
 FILING DATE: January 12, 1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/928.464
 FILING DATE: August 10, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Lori Y. Beardsell
 REGISTRATION NUMBER: 34,293
 REFERENCE/DOCKET NUMBER: UPN-1108
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3033 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 118..2583
 US-08-003-311B-1

Alignment Scores:
 Pred. No.: 3,066-272 Length: 3033
 Score: 2742.50 Matches: 546
 Percent Similarity: 73.63% Conservative: 99
 Best Local Similarity: 62.33% Mismatches: 144
 Query Match: 61.84% Indels: 87
 DB: 1 Gaps: 14

US-09-904-389-2 (1-850) x US-08-003-311B-1 (1-3033)

Qy 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
 Db 118 ATGGAATGCCGGTAGAAGATCTAATTACACTTTGCTTAGTCAATTTTCTGACGATCAG 177
 Qy 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
 Db 178 GTGTGAGTTTCGTACCCGAGCTCCTCCGCTCCTACTATGATTCCTTGTGAGCGGAAAC 237
 Qy 36 -----GlyGlyAsnValIleLysGlyAArgThrAspArg---ValPheAsp 49
 Db 238 AGGAGCAACCAACAGCGGGAACCCGGGAAGCTTAAGCGGAGAGCGGATTTGAT 297
 Qy 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
 Db 298 TGGGATCCTAGCGGTGGTGGTGTGATCATAGTTGGAATAATCAACCGAATCGGGTT 357
 Qy 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
 Db 358 GGGATATATATGATGCTTCGTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 417
 Qy 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
 Db 418 GGTGAGAGCTCTTTGTCTGGGGATTATTACATGCTTCTCT---CGCGCGCTAAC 474
 Qy 104 GluIleAsnAlaLeuGlnTyrIleLeuAspAspPheArgVal----- 118
 Db 475 GAGATCGAACTCTGTGGATTCTCTCAAGATGATGGGTTTAGCTTGGATTGGTGGT 534

Qy 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
 Db 535 CGAGGAGATTGAGGATACAGATGGCGGAGACTCCGCTGGAGGGTCTTCATCTGGGAG 594
 Qy 131 SerTrpAlaGlnGlnThrGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
 Db 595 AGCTGGCGCAGCAGACGAGGAGAGTATCAGCTGAGCTTGCATTGGCGTTAAGGCTT 654
 Qy 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
 Db 655 TCGTCGGAGGCTACTTGTGCGCAGATCCGAATCTTCTGGATCTCTACCGGACGAGTCT 714
 Qy 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190
 Db 715 GCTTTACGGAATTCGCAAGTTTCAGCCGAAACCGTTTCACATCGTTCTGGGTTAATGCG 774
 Qy 191 CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro 210
 Db 775 TGCATTATCGTACTATGATAAGTTCTCTGATGGGTTTATATGATGAATGGTCTGGATCCC 834
 Qy 211 TyrValTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer 230
 Db 835 TATATTGGACCTTATGATCGACCTGCATGAAAGTGTGCGATCCCTTCAATTGAATCA 894
 Qy 231 LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis 250
 Db 895 TTAGAGCTGTTGATTTCTGGTGTGATTTCTTCGCTTGAAGCGATCATAGTTGATAGCGT 954
 Qy 251 SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysVal 270
 Db 955 AGTGATCCAGCTTCAAGAACTTCACATAGATGCCAGCATATCTTGTAGCTGAT 1014
 Qy 271 ThrThrLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlySer 290
 Db 1015 ACCACAAAAGAGTTGTTGATCAGCTGCGAAAGCTTATCTGCAATCGTATGGGGTCCA 1074
 Qy 291 ValSerGluGlyGluAspAspLeuValSerAlaTrpLysGluCysSerAspAspLeuLys 310
 Db 1075 GTTATCATGGGGAGATGAGTTGGTCCCATGTTGGAGGAGTGCTTGAATGGTCTAAAA 1134
 Qy 311 GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis 330
 Db 1135 GAA---ATCTTTAAAGTGTGTTCCCATAGTAGTACCTCTCTGTTGACTCTGCAGACAT 1191
 Qy 331 ArgAlaLeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys 350
 Db 1192 CGAGCTTTACTCTTCAAAGTACTGCTGACATAATTGATTACCTCTCGAATTGCCAAA 1251
 Qy 351 GlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPheGlyLeuAsp 370
 Db 1252 GATGTAAATATTGTAAAGACGATGCCGCTTCGTGCTTGTTCAGTTTGGCTTGAT 1311
 Qy 371 ArgGluTyrLeuIleAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeu 390
 Db 1312 AGGAGTACCTGGTTGATTATTAGTAAGAACGACGCTCACTTATGGGAGCTGATTCCTTG 1371
 Qy 391 LeuAsnGlyProSerSerIleSerIleSerProLeuArgPheProArgLeuLysPro 410
 Db 1372 CTAATGTCTTCTTCACTATCTCAATTTCTCTCTCTGGGTTTCCAGCAACCAAGCCA 1431
 Qy 411 IleGluSerThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSer 430
 Db 1432 GTTGAACCGCAGTCGATTTTAGTTAGTTACTGCCAAACAATATTTCTCCGATAGCAGTCT 1491
 Qy 431 LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla 450
 Db 1492 CTTAATCTGTTTTCGATCCCTGCATCAGT-----GATATGGGA 1530
 Qy 451 PheSerValTyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal 470
 Db 1531 TTCTCAATGTTTTCATAGCAATATGATAATCCGGGTGGAGAGATGACGATTCGGCAGAA 1590

QY 471 ThrGlyAspLysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThr 490
Db 1591 AATGGTGGT----- 1599
QY 491 GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
Db 1600 -----GGGTCT 1605
QY 511 ThrProPheValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAsp 530
Db 1606 TTGCCACCCAGTCTAATATGCTCCA----- 1632
QY 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe 550
Db 1633 ---CAGACATGATGGTGGTCAATCAATCAATGAAGCAGCAGCCTATGATGCCCCACCA 1699
QY 551 ValHisGlySerGlnLeuLeuArgLysProAsnGluLeuSerGlyLeuGluAspLeu 570
Db 1690 ATCAGTCAGCCAGCTTCCAAACAGGCGCAATAGGAACTTGGAGCTTGATGGTGATGATG 1749
QY 571 ValIleProThrPheAspLeuAspLeuArgGluLysIleGlyValAlaGlySerPheGlyThr 590
Db 1750 GACATCCCGGGTGTGATCTTATATATAAGAAAGATTGGAGCAGGTTCCTTGGCACT 1809
QY 591 ValTyrArgGlyGluThrHisGlySerAspValAlaValLysIleLeuThrGluGlnAsp 610
Db 1810 GTCCACCGTGTGAGTGGCATGGCTGGATGTTGCTGTGAATAATCTCATGGAGCAAGAC 1869
QY 611 PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg 630
Db 1870 TTCCATGCTGAGCGTGTATGATGATGTTCTTAAGAGAGTTGCCGATATGAAGCGCTTGGC 1929
QY 631 HisProAsnIleValLeuPheMetGlyAlaValThrLysProAsnLeuSerIleVal 650
Db 1930 CACCCTAATGTTCTCTTCTCATGGGTCGCTCACTCACTCCAAATTTGCAATAGTG 1989
QY 651 ThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAsp 670
Db 1990 ACAGAAATTTGTCAAGAGGTGATTTATACAGACTTTGCTATTAAGTGGACAGGAG 2049
QY 671 ---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr 689
Db 2050 CAATTAGATGAGAGCTGGCTGAGTATGGCTATGATGCTGCTAAGGGAATGATAT 2109
QY 690 LeuHisArgArgAspProIleValHisArgAspLysSerProAsnLeuLeuVal 709
Db 2110 CTTCACAAATCCCAATCTCCAAATTTGCTAGAGATCTAAATCTCCAACTTATTTGGT 2169
QY 710 AspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThr 729
Db 2170 GACAAAAATATACAGTCAAGTGTGATTTGTTGTTCTCTCGCGATTGAAGGCCAGCAG 2229
QY 730 PheLeuSerSerLysSerAlaAlaGlyThrProGluThrMetAlaProGluValLeuArg 749
Db 2230 TTTCTTTCTCGAAGTCAGAGCTGGAGTCCCGGAGTGGATGGCAGAGTCTGGCA 2289
QY 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrGluLeu 769
Db 2290 GATGAGCGGTCTAATGAAGAAGTCAGATGTGATACAGCTTCGGGTCTCTTGTGGAGCTT 2349
QY 770 AlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValValAlaAlaValGly 789
Db 2350 GCTATATTGCAACCAACCTAGGCTAACTTAATCCGCTCAGGTGTAGCTGGGTGGT 2409
QY 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle 809
Db 2410 TTCAAGTGTAAACGGCTGGAGTCCCGGTAACTCTGAATCTCAGGTGGCAGCATATC 2469
QY 810 ValAlaCysTyrAlaAspGluProTyrLysArgProSerPheSerIleMetGluThr 829
Db 2470 GAGGGTGTGGACCAATGAGCCATGAGCGTGGTCCATCTTTCGAATATAATGAGTGTG 2529
QY 830 LeuLysProMetThrLysGlnAlaProGlnGlnSerArgThrAsp 845

Db 2530 CTAGACACCATGATCAATCAGCGGTTCTCCGCCCAACCGCTCGGAT 2577
RESULT 4
US-08-261-432-1
Sequence 1, Application US/08261432
Patent No. 5602322
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261.432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003.311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..2593
US-08-261-432-1
Alignment Scores:
Pred. No.: 3,06e-272 Length: 3033
Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: Gaps: 14
US-09-904-389-2 (1-850) x US-08-261-432-1 (1-3033)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 118 ATGGAATGCCCGGTAGAAGATCTAATACACTTCTGCTTAGTCAATTTCTGACGATCAG 177
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaIle----- 35
Db 178 GTGTCAGTTTCCGTCACCGGAGCTCTCCGCTCACTATGATTCCTTGTCTGAGCGGAAAC 237
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg--ValPheAsp 49
Db 238 AGGAGCAACCAATAACAGCGGGAACACCGGGAAGAGCTAAGCGGAGAGAGCGGATTTGAT 297


```
Db 2290 GATGAGCCGCTTAATGARAAGTCAGATGTGTACAGCTTCGGGGTCATCTTGTGGAGCTT 2349
Qy 770 AlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnValAlaValGly 789
Db 2350 GCTACATTGCAACACCATGGGGTAACTTAAATCCGGCTCAGGTGTAGCTGCGGTTGGT 2409
Qy 790 PheLeuGlyLeuArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle 809
Db 2410 TTCAAGTGTAAACGGCTGGAGATCCCGGTGAATCTGAAATCCTCAGGTGCAGCCATAATC 2469
Qy 810 ValAlaCysTrpAlaAspGlnProTrpLysArgProSerPheSerSerIleMetGluThr 829
Db 2470 GAGGGTGTGGACCAATGAGCATGGAAGCCATCATTTGCAACTATATGACATTG 2529
Qy 830 LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp 845
Db 2530 CTAAGACCATGTCAATCAGCGGTTCCTCCGCCAACCGTCGGAT 2577

RESULT 5
US-07-928-464-3
; Sequence 3, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieker, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065-ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1..353
; FEATURE:
; NAME/KEY: exon
; LOCATION: 354..1001
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1002..1176
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1177..1477
; NAME/KEY: intron
; LOCATION: 4883..4959

; LOCATION: 1478..1574
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1575..1719
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1720..1936
; NAME/KEY: exon
; LOCATION: 1937..2038
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2039..2173
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2174..2379
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2380..2736
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2737..3012
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3013..3202
; NAME/KEY: exon
; LOCATION: 3203..3243
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3244..3519
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3520..3588
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3589..3668
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3669..3769
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3770..3858
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3859..3943
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3944..4037
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4038..4136
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4137..4369
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4370..4438
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4439..4541
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4542..4673
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4674..4787
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4788..4882
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4883..4959
```


403	LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys	422
2268	CTGGCGTTTCCACGACCAAGACGATGAAACCCGACGCGATTTAGGTCTACTAGCCAAA	2327
423	GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer	439
2328	CAATAATTTCTCCGATAGCCAGTCTCTTAATCTGTGTTTTCGATCTCGCATCAGGTATTCCC	2387
439	-----	439
2388	ATACAAAAAACCTGAATATATATGTTAACTTTTGGCATGCTGTACATCTCGTTTGTAT	2447
440	-----SerGlyAsnValValSerGlyLysAspAlaIaPheSerValTyrGlnArg	456
2448	TTCCCTCTAAAGAGTAAATCTCTATCA-----TTTAGGGTATTT	2486
457	ProLeuAsnArgLysAspValAspGlyLysThrIleVal	469
2487	---CTTGATCATGCTCAGTATCTGAAGCTGTAGTAGTCTTAGAATGATTCTATTGTTTG	2543
470	-----ValThrGlyAsp	473
2544	TTTTCTTGCTCTTTTCACTTTTAACTTTAGTTTGGCTGTTCATGCTGTATGTTGTGGTG	2603
474	-----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaIa	486
2604	GTTCTTTGGCTAATGATATTTAAGTTTAACTTGTAGTCTGCTGTTCAAG	2654
487	GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty	506
2655	---CTTATGAATCTAGTGCAATTTATGTGCAAGACTTGCTCTCGGACTCTAAT	2705
506	rSerVal-----GlnSerThr-ProPheValG1	515
2706	TTCATTATATCTGCTGTTGAATGGTGTAGATCATATCGGATTTCTCAATGTTTCATAGG	2765
515	uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisIle	534
2766	CAATATGATAATCCGGGTGGAGAGAAATGACGCATGG-----CAGAAAATGCT	2813
534	uLeuAlaLeuSerHisProArgMet-----	542
2814	GGTGGGCTTTGCCACCCAGCTGCTTAATAGCTCCACAGAACATGATGCGTGCGTCAAAAT	2873
543	-----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLys	559
2874	CAAAATTGAAGCAGCACCTTATG- AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGC	2932
559	sProAsnGlnLeuSerLeuGlyLeuGluAspLeuValIleProIleThrAspLeuAspLeu	579
2933	AAATAGGAACTTGACCTTGATGGTGATGATATGGACATCCCGGTGGTGATCTCTTAATAT	2992
579	uArgLysIleGlyAla-----	585
2993	AAAAAGAAAGATTGGAGCAGGTAAATTTTACGAAAAAATAATGATTCCGCTCAAAA	3052
585	-----	585
3053	TGCAAGAAATATGAATTTCTTGAGGAAGTGGTTTGGTCTGTTGGACTCTGTTCTCGAACAA	3112
585	-----	585
3113	AATAAGGAAAAAGTCCACCCATTTTGATTTACATTTCTCTGTGGCTTTAAATCTTT	3172
586	-----GlySerPheGlyThrValTyrArgGlyGlnT	596
3173	CCACTCTAATTTGAGGACTGCTCTTTGAGGTTCTCTTGGCAGCTGTCTCCACCGTCTGAGT	3232
596	rHisGlySer-----	599
3233	GGCATGGCTCGGTAAAGAACTTTTGTGCAGAAATTTACGAGCTGAATTTTTTTTGGCTCT	3292
599	-----	599

Db	3293	AAAAATTGGTTGGACTTTTGGATCTCTGGTATTATAAAAGGCAAAAGTTATTGTATA	3352
QY	599	-----	599
Db	3353	TGTGACTCTCCGTTCTGTCAGAAATTAACACGACGACAAAGGTGCCATTTTAGATGA	3412
QY	599	-----	599
Db	3413	TATGTGCTTTTATATCATAAATTTCTCTCTGTTTGAATTTTACAATTCATCATAGA	3472
QY	600	-----AspValalaVal	604
Db	3473	AGAAATCTAAATTTTGATTATTCAGTAATATCTCTATCAATTTTCAGGATGTTGCTGTGA	3532
QY	604	ysIleLeuThrGluGlnAspPheHisProGluuArgValasnGluPheLeuArgGluVal-	623
Db	3533	AAATTTCTCATGGACGAAGACTTCCATGCTGACGCGTGTAAATGAGTCTTTAAGAGAGGT-G	3591
QY	623	-----	623
Db	3592	CACAAATAAAATTTCTCTTGATTTTGGTAATGAACCTTTGTTGATTAAATGCTCTCCAATGA	3651
QY	624	-----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP	637
Db	3652	TCTTGATTTCGCTGTCAGGTTGGGATGAATGAACGGCTTCGCCACCCATAACATTTGTTCTCT	3711
QY	637	heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrieuSer	655
Db	3712	TCATGGGTGGCTCACTCAACCTCCAAATTTCTCAATAGTGACAGAATATTGTGC-AAGG	3770
QY	655	-----	655
Db	3771	TACAATTACTTGGATTTGGAAAGTTTGTATGTAAGTGTAGAAATTTTGGCCTTAATAGA	3830
QY	656	-----ArgGlySerLeuTyArgLeuLeuHisLysSerG	667
Db	3831	CTCTAATACCATGATTTCTTTCAAACAGAGGTAGTTTATACAGACTTTTGCATAAAAGTG	3890
QY	667	lyValLysAsp---IleAspGluThrArgArgIleasnMetAlaPheaspVal	683
Db	3891	GAGCAAGGGACAAATTAGATGAGAGACGTCGCTGATGATGGCTTATGATGTGGTATGTT	3950
QY	683	-----	683
Db	3951	TAACCTCCTTATGTACATGTATGGTGATTTACTTCTGTATCTTGGTGTCTTTCACATGG	4010
QY	684	-----AlaLysGlyMetAsnTyLeuHisArgArgasp	694
Db	4011	AACTTTCTTTCCAAATCTCTGTACAGCTTAAGGAATGAATATCTTCACAAATCGCAAT	4070
QY	695	ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyThr	714
Db	4071	CCTCCAAATTTGTGCATAGAGATCTAAATCTCCAAACTTATTGTTGTTGACAAAAAATATACA	4130
QY	715	valLysval-----	717
Db	4131	GTCAAGGT--TTGAATCTAAATTAGAAATTTGTTGTGCCAATGTTTGTATTTTGATATTTT	4189
QY	717	-----	717
Db	4190	ATTCCTCTTTGTCAGACAAGCTTATATATAAATTATGATTTTAAATTTCTAAATTTGGT	4249
QY	717	-----	717
Db	4250	AGACATTACAAAAGCGTTAATCTGCTGAAACTTAAGATACACGACCTCAAGCTGT	4305
QY	717	-----	717
Db	4310	CGTCTTAAAAAACAATCAGAACATTATTATTCTAACTCCTCAATTTTGTCTTGAAATTCAG	4365
QY	718	---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla	736

Db 4370 GTTGTGATTTGGTCTCTCGGATTGAAGCCAGCAGGTTCTTTCTCTCGAAGTCAGCA 4429
QY 737 AlaGlyThr----- 739
Db 4430 GCTGGAACCGTAAGTTCAGTTGTTTGAACATAAAACACGCTGAACAACGTAACCTTCTT 4489
QY 740 -----ProGluTr 742
Db 4490 CTAGGTCCTATTTCCTCAATGGAAGCTAAATAATTAAGTCTGTTGATATATCAGCCCGAGTG 4549
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluYsSerAspValTrSerPh 762
Db 4550 GATGGCACCAAGTCTCTCGAGATGAGCCGCTCTAATGAAAGTCAGATGTGTACAGCTT 4609
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGluProTrpCysAsnLeuAsnProAl 782
Db 4610 CGGGGTCATCTTGTGGAGCTTGCTACATGCAACACCATGGGGTAACCTTAATCCGGC 4669
QY 782 agln----- 783
Db 4670 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATATATTTTGCATTGGAAGT 4729
QY 784 -----Va 784
Db 4730 CCTCACTCTCAATTCATAACATCATATATATATATATATATATATATATATATATATAT 4789
QY 784 lValAlaAlaValGlyPheGlyArgLeuAspGluProArgAspValAsnProLy 804
Db 4790 TGTAGCTGGGTGGTTTCAAGTGAACGGCTGGAGATCCGGTAACTCTGATCTCTCA 4849
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 4850 GGTTCGACCAATAATCGAGGGTGTGTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTT 4908
QY 815 -----AspGluProTr 818
Db 4909 TTCAATCTTCTTGAATAGACTTCATGTTATGATGTGTTTCAATACCAGTGAGCCATG 4968
QY 818 plysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 4969 GAAGCGTCCATCATTTGCAACTATAATGACTTGTCTAAGACCATTTGATCAATCAGCGGT 5028
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5029 TCCTCGCCCAACCGCTCGAT 5050

RESULT 6

PCT-US93-07347-3
; Sequence 3, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Kieber, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347
; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1..353
; FEATURE:
; NAME/KEY: exon
; LOCATION: 354..1001
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1002..1176
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1177..1477
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1478..1574
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1575..1719
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1720..1936
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1937..2038
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2039..2173
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2174..2379
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2380..2736
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2737..3012
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3013..3202
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3203..3243
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3244..3519
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3520..3588
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3589..3668
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3669..3769
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3770..3858
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3859..3943
; FEATURE:

```

NAME/KEY: intron
LOCATION: 3944..4037
FEATURE:
NAME/KEY: exon
LOCATION: 4038..4136
FEATURE:
NAME/KEY: intron
LOCATION: 4137..4369
FEATURE:
NAME/KEY: exon
LOCATION: 4370..4438
FEATURE:
NAME/KEY: intron
LOCATION: 4439..4541
FEATURE:
NAME/KEY: exon
LOCATION: 4542..4673
FEATURE:
NAME/KEY: intron
LOCATION: 4674..4787
FEATURE:
NAME/KEY: exon
LOCATION: 4788..4882
FEATURE:
NAME/KEY: intron
LOCATION: 4883..4959
FEATURE:
NAME/KEY: exon
LOCATION: 4960..5056
FEATURE:
NAME/KEY: intron
LOCATION: 5057..5890
PCT-US93-07347-3

Alignment Scores:
Pred. No.: 1,22e-202
Score: 2072.00
Percent Similarity: 41.83%
Best Local Similarity: 34.92%
Query Match: 46.72%
DB: 5
Gaps: 34

US-09-904-389-2 (1-850) x PCT-US93-07347-3 (1-5890)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 354 ATGGAAATGCCCGTAGAAGATCTAATTACACTTTGCTTAGTCAATTTCTGACGATCAG 413
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAala----- 35
Db 414 GTGTGAGTTTCGGTCACCGGAGCTCCTCCGCTCAGTATGATTCCTTGTCGAGCGAAAC 473
QY 36 -----GlyGlyAsnValIleLeysGlyArgThrAspArg---ValPheAsp 49
Db 474 AGGAGCAACATAACAGCGGGAACACCGGAAAGCTAAGCGGAGAGAGCGGATTTGAT 533
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 534 TGGGATCCPAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 593
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 594 GGGATAATATGATGCTTCGCTCTAGGTTGCCAAGCAATCCAGTGGGAGTAGTTTC 653
QY 84 AspAspSerSerLeuSerSerAspTyrTrpAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 654 GTTGAGAGCTCTTGTCTGGGATATTACATGCGCTACGCTTCT---GCGGCGGCTAAC 710
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
Db 711 GAGATCGAATCTGTGGATTTCTCAAGATGATGGGTTTAGCTTGGATTTGGGTGGT 770
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130

```

```

771 GGAGGAGATTTGAGGATACAGATGGCGCGGACTCCCGCTGGAGGGTCTTTCATCTGGGAAG 830
131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
831 AGCTGGCGCAGCAGCAGGAGAGATTATCAGCTGCAGCTTGCAATTGGCGTTAAGGCTT 890
151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
891 TCGTCGGAGCTACTTGTGGCGACATCCGAACCTTCTGGATCTCTACCGGAGAGATCT 950
171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
951 GCTTTACGAGCTTCGCCAAGTTCACCGCAACCGTTTCACATCGTTTCTGGGTATTGTT 1010
187 ----- 187
1011 CCGTTTAAGCTTTGTTTCCAAAATATTGAATCGTGGTTATAGAGATATGCTCTCTTG 1070
187 ----- 187
1071 TTTCCGAAGTTTCAGTTAGATCTCCTTACCAAAAGCTTATTAGTAGCAAAATGAGATATGT 1130
188 -----ValAsnGlyCysMe 192
1131 TGTTTAGATACATTGCAGAGATATGATTTGTTGTGCTGCTGCATCAGGTTAATGGCTGCTT 1190
192 tSerTyrLeuGluLeuValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
1191 ATCGTACTATGATAAAGTTCTGTGAGGTTTATATGATGAATGCTGTGATCCCTATAT 1250
212 tTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLys 232
1251 TTGAGCCTTATGATCGATCGATGAAAGTGGTGGCATCCCTCAATGAATCAATTAAAG 1310
232 sThrValAspSerIleGlySerSerIleGlyValValLeuIleAspArgHisSerAs 252
1311 AGCTGTGATCTCGGTGTGATCTTCGCTTGAGCGGATCATAGTTGATGGCGTAGTGA 1370
252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
1371 TCCAGCCTTCAGGAACCTTCACAATAGATGCCACGACATATCTTGTAGCTGCATTACCC 1430
272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
1431 AAAAGAGTTGTTGATCAGCTGSCAAAGCTTATCTGCAATCGTATGGGGTTGTACTCAT 1490
288 ----- 288
1491 ACAATCCTTACTATCCCTTTGAACTTATATTTTATATCTTCTGTGATTTCTCATTTG 1550
289 -----GlySer-ValSerGluGlyGluAspAspLeuVal 300
1551 TACTCGTTAATCTTGTCTCCCGAGGGTCCAGTTATCATGGGGNAGATGATGTTGGTTC 1610
300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
1611 CCATGTGGAAGGAGTGCATTGATGGTCTAAAGAA---ATCTTTAAAGTGGTGGTTC 1667
320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
1668 TAGGTAGCCTCTCTGTTGGACTCTGCGAGATCGAGCTTACTCTTCAAGTGAGATCCC 1727
336 ----- 336
1728 AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAATGATCATATAAATTATT 1787
336 ----- 336
1788 GTGCTTTCATCCATTTGTTTTTATTGGGAATACATATGAAGAACCTTGAAATGTGAAAAAGTGG 1847
336 ----- 336

```


Db 1848 TGTATTGATTAGAAAAAATAGGTTACTGATAGTTGAATGTTCCAAAGAAAAAAGATAT 1907
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 1908 TTATATCTTCTATTGTTGGTGCATGCAGGTACTGCTGACATAATTGATTACCTTCGA 1967
QY 348 lleAlaLysGlyCysLeuTyCysThrArgAspAlaSerSerCysLeuValArgPhe 367
Db 1968 ATTGCCAAAGGATGAAATATTGTAATAGACAGCATCGCTTCGTGCCTTGTCAAGTTT 2027
QY 368 GlyLeuAsp----- 370
Db 2028 GGGCTTGATAGTATGACAAAGTATGCCAAGAGCCATTATTTTCCTATTTCCTTTC 2087
QY 370 ----- 370
Db 2088 CTTTTTGTTCGAAAAACAATTATAGCTCCAAATGTTTCGAGAATAATTAGTTGATG 2147
QY 371 -----ArgLufyLeuIleAspLeuIleGlyAspProGly 382
Db 2148 AGCTGAAAAATTGTTGGTTTCAGGAGTACTGTTGATTATTAGTAAAGACGAGT 2207
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerIleSerIleSerSerPro 402
Db 2208 CACTTATGGAGCCTGATTCTTGTGTAATGCTTCATCTATCTCAATTCTCTCCT 2267
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2268 CTGCGTTTCCACGACCAAGCCAGTCGATGACCCGAGTCGATTAGTTAGTACTAGCCAA 2327
QY 423 GlnTyPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer----- 439
Db 2328 CAATATTTCTCGATAGCCAGTCTCTTAATCTGTTGTTTCGATCCTGCATCATCGATTCC 2387
QY 439 ----- 439
Db 2388 ATACAAAAACCTGAATATATGTAATCTTTTTCAGTCTGCTTACATCTCGTTTGTAT 2447
QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyGlnArg 456
Db 2448 TTCCCTAAAGAGTAATCTCTATCA-----TTTAGGTATTI----- 2486
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
Db 2487 ---CTTGATCATGCTCTCAGTATCTCAAGTGTAGTAGTCTTAGAATGATTCATTGTTG 2543
QY 470 -----ValThrGlyAsp----- 473
Db 2544 TTTTCTGTCTCTTTTCACCTTTAGTTGTTTGGCTGTGATGCTATGTTGTTGGTGG 2603
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 2604 GTTCTTTGGCTAATGATATTAAAGTTAAACTTGTAGTCTGCTGTTCAAG----- 2654
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheAspSerCysValAlaAspPro-Ty 506
Db 2655 -----CTTATGAATCTAGTCAATTATGTGCAAGACTTGTCTCTGCATCTAAT 2705
QY 506 rSerVal-----GlnSerThrProPheValGI 515
Db 2706 TTCTTATATCTGCTTTGTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG 2765
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 2766 CAATATGATAATCCGGTGGAGAGATAGCCATTGG-----CAGAAATAGGT 2813
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 2814 GGTGGTCTTTGGCCACCCAGTGTATAATGCTCCACAGAACATGATCGGTGCTCAAA 2873
QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLys 559
Db 2874 CAAATTGAAGCAGCACCTATG-AATGCCCCCAACAATCAGTCAGCCAGTTCACACAGGGC 2932

QY 559 sProAsnGluLeuSerIleuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLe 579
Db 2933 AAATAGGAACTTGGACTTGCATGCTGATATGACATCCCGTGTGTGATCTTAATAT 2992
QY 579 uArgGluLysIleGlyVala----- 585
Db 2993 AAAAGAAAAGATTGGACAGGTAAATAATTTACGGAAAAAATAATGATTCGGTCTAAAAA 3052
QY 585 ----- 585
Db 3053 TGCAAGAAATATGAATTTCTGAGGAAGTGGTTTTCCTTGGACTCTGTTCTCGAACAA 3112
QY 585 ----- 585
Db 3113 AATAAGGAAAAAGTGCCACCCANTTTTGAGATTACATCTTCTGTTGCTTAAATCTT 3172
QY 586 -----GlySerPheGlyThrValTyArgGlyGluT 596
Db 3173 CCACCTCTAAATTGAGCGAGTCTCTTTTCAGGTTCTTTGGCACTGTCCACCGTCTGAGT 3232
QY 596 rPHisGlySer----- 599
Db 3233 GGCATGGCTCGGTAAAGAACTTTTGTGAGAAATTACGACGCTGAATTTTTCCTCTCT 3292
QY 599 ----- 599
Db 3293 AAAAATTGGTTGTGACTTTTGGATCTGCTTGTGATTATATAAAGGCAAGATTATTCTATA 3352
QY 599 ----- 599
Db 3353 TGTGACTCTCGTTCTGTGAGAAATTAAACACGACAAAAGGTGCCCATTTTAGATGTA 3412
QY 599 ----- 599
Db 3413 TATGTGCTTTATATCATAAATTGTCTCTCTGTTGAATTTTACAATTCATCACTAGA 3472
QY 600 -----AspValAlaVal 604
Db 3473 AGAATCTCAATTTTGTATTTCAGTAATAATCTCTATCAATTCAGGATGTTGCTGTGA 3532
QY 604 yAlleLeuThrGluGluAspPheHisProGluArgValAsnGluPheLeuArgGluVal- 623
Db 3533 AAATTTCTCATGAGCAAGACTTCCATGCTGAGGCTGTATAGAGTCTTTAAGAGAGGT-G 3591
QY 623 ----- 623
Db 3592 CACAAATAAATTTTCTCTGATTTTGGTAATGAACCTTGTGTATTAAATGCTCCAATGA 3651
QY 624 -----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
Db 3652 TCTTGATTCGCTGTGAGTTGCGATTAATGAACGCTTCGCCACCTTACATTTGTTCTCT 3711
QY 637 heMetGlyAlaValThrLysProAsnLeuSerIleValThrGluTyLeuSer----- 655
Db 3712 TCATGGGTGCGTCACTCAACCTCCAAATTTGTCAATAGTCACAGAAATATTTGTC-AAGG 3770
QY 655 ----- 655
Db 3771 TACAATTACTTGGATTGGAAAGGTTTGATGTACTGAGTGTAGAAATTTTGGCCTATAATGA 3830
QY 656 -----ArgGlySerLeuTyArgLeuLeuHisLysSerG 667
Db 3831 CTCATAATACCATGATTCTTTCACACAGAGGTAGTTTATACAGACTTTTGCATAAAAGTG 3890
QY 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetalapheAspVal----- 683
Db 3891 GAGCAAGGAGCAATTAGATGAGAGACGTCGCTGAGTATGGCTTTATGATGTGTATGTT 3950
QY 683 ----- 683
Db 3951 TAATCTCTTATGTTACATGATGGGTGATTACTTCTGATCTTGGTGTCTTCTTCACATGG 4010

```

QY 684 -----AlaLysGlyMetAsnTyrLeuHisArgAsp 694
Db 4011 AACTTCTTCCAAATCTCTGTCACAGGCTAGGGAATATCTTTCACAAATCGCAAT 4070
QY 695 ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr 714
Db 4071 CTTCCAAATTTGTGATAGATCTAAATCTCCAAATCTTATTTGGTTGACAAAATATATACA 4130
QY 715 ValLysVal----- 717
Db 4131 GTCAGGT-TTGAATCTAAATTAGAAATTTGTGTCTCCAAATTTTGTATTTT 4189
QY 717 ----- 717
Db 4190 ATTCTCTTGTGAGACAAGCTTATATATAAATATGATTTTTTAATCTAAATTTGGTGG 4249
QY 717 ----- 717
Db 4250 AGACATTACAAAAGGGTTAATCTCTGAAACTTAAAGATACAGCAGCTCAGCTGT 4309
QY 717 ----- 717
Db 4310 CGTCTTAAAAACAATCAGAACATTATTATTCTCAACTCTCAATTTGTCTTGAATTTTCAG 4369
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4370 GTTTGTGATTTTGTCTCTCGCATTTGAAGCCGACGCTTCTTCTTCTCGAAGTCAGCA 4429
QY 737 AlaGlyThr----- 739
Db 4430 GCTGGAACCGTAAGTTCAGTTTGTGTTGAAACTAAACAGCTGAACAGTAACCTTCTT 4489
QY 740 -----ProGluTr 742
Db 4490 CTAGTCTCTATTTCCAAATGAAGTAATTAATTAATGACTTTGATATATACCCCGAGTG 4549
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4550 GATGCGACCAAGACTCTCGAGATGAGCGCTCTAATGAAAGTCAGATGCTGTACAGCTT 4609
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnProTrpCysAsnLeuAsnProAl 782
Db 4610 CGGGGTCACTTGTGGGAGCTTGTACATTGCAACACCAATGGGTAACTTAAATCCGCG 4669
QY 782 agln----- 783
Db 4670 TCAGTACTTCCACTCTAAACATCCCAATAATAATGATATATTTTTCATTTGGAAGT 4729
QY 784 -----Va 784
Db 4730 CCTCACTCTACATTTTCAATGCTATATATGATCATCCAAACAAATGTTCCATAGT 4789
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 4790 TGTAGCTGGGTTGGTTTCAAGTGTAAAGCGCTGAGATCCCGGTAATCTGAATCCTCA 4849
QY 804 sLeuAsSerLeuIleValAlaCysTrpAla----- 814
Db 4850 GGTTCAGCCATAATCGAGGTTGTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 4908
QY 815 -----AspGluProTr 818
Db 4909 TTGAATCTCTTGAATAGACTTCATGTTTATGTTATGTTTTCATTACCAAGTCAGGCAATG 4968
QY 818 pLysArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 4969 GAAGCGTCCATCATTTTGAACATATATGACTTGTCTAAGACCATTTGATCAATCAGCGGT 5028
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5029 TCTTCGCCCCAACCGCTCGAT 5050

```

RESULT 7

```

US-08-003-311B-3
; Sequence 3, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSES: No. 5444166ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-003-311B-3

```

```

Alignment Scores:
Pred. No.: 1,37e-202 Length: 6312
Score: 2072.00 Matches: 556
Percent Similarity: 41.83% Conservative: 110
Best Local Similarity: 34.92% Mismatches: 159
Query Match: 46.72% Indels: 772
DB: 34 Gaps: 34

```

```

US-09-904-389-2 (1-850) x US-08-003-311B-3 (1-6312)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 776 ATGGAAATCGCGGTAGAGATCTAATTACACTTTGCTTAGTCAATTTTCTGACGATCAG 835
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 836 GTGTCAGTTTCCGTCACCGGAGCTCTCCGCTCACTAIGATTCCTTGTGAGCGGAAAC 895
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 896 AGGAGCAACCATACACGCGGAAACACCGGAAAGCTAAGCGGAGAGAGCGGATTTGAT 955
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 956 TGGGATCCTACCGGTGTGTGTGTGTGATCATAGTTGAATATACCGAATCGGTT 1015
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83

```

Db 1016 GGAATAATATATGATGCTTCTGCTCTAGGGTTGCAAGGCAATCCAGTGGAGTAGTTTC 1075
Qy 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 1076 GGTGAGAGCTCTTTGTCTGGGATTAATACATGCTACGCTTTCT---GGCGGGCTAAC 1132
Qy 104 GluLeuAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal-----118
Db 1133 GAGATCGAATCTGTGGATTTCTCCTCAAGATGATGGTTTAGGCTTGGATTTGGTGGT 1192
Qy 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 1193 GGAGGAGATTTGAGGATACAGATGCGCGGCGACTCGCTGGAGGCTTTCATCTGGGAAG 1252
Qy 131 SerTrpAlaGlnGlnThrGluGlnSerPheGlnLeuGlnInProLeuValLeuArgLeu 150
Db 1253 AGCTGGCGCAGCAGCAGGAGAGATTATCAGCTGCAGCTTGATTCGGCTTTAAGGCTT 1312
Qy 151 SerSerAsp***ThrCysAlaAspProAsnPheMetAspProIleProAspGluAla 170
Db 1313 TCGTCGGAGCTACTTGTGCGCAGCATCCGAACCTTCTGGATCCTGTACCGAGAGTCT 1372
Qy 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp-----187
Db 1373 GCTTACGGACTTCGCCAAGTTTCAGCGAAACCGTTTCACATCGTTCTCGGATTTGTT 1432
Qy 187 -----187
Db 1433 CTGTTTAAGCTTTGTTCCCAAAATTTAATGAATCGTGTATAGAGATATGCTCCTTGG 1492
Qy 187 -----187
Db 1493 TTTCCGAAGTTTCAGTTAGATCTCCTTACCAAAAGTCTATTAGTAGCAAAATCAGATATGT 1552
Qy 188 -----ValAsnGlyCysMe 192
Db 1553 TGTTTACATACATTCGAGAGTAGATGTTTGTGTGTGCTGCATCAGGTTAATGCTGCTT 1612
Qy 192 tSertYrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
Db 1613 ATCGTACTATGATAAAGTTCCCTGATGGGTTTATATGATGAATGCTCGGATCCCTATAT 1672
Qy 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232
Db 1673 TTGGACCTTATGATCGACCTGCATGAAGAGTGGTCCGATCCCTTCAATGAATCATTAA 1732
Qy 232 sThrValAspSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
Db 1733 AGCTGTTGATTTCTGGTGTGATTTCTTCGCTTGAAGCGATCATAGTTGATAGCGTAGTGA 1792
Qy 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
Db 1793 TCCAGGCTTCAAGGAACCTTCACAAATAGAGTCCAGCACATATCTGTAGCTGCATTACCAC 1852
Qy 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly-----288
Db 1853 AAAAGAGTTTGTGATCAGCTGCGAAGGCTTATTCGAATCGTATGGGGTTTGTACTCAT 1912
Qy 288 -----288
Db 1913 ACAATCCTTACTACCTTTGAACCTTATATTTTATATCTCCTGTGATTTCTCACATTTG 1972
Qy 289 -----GlySer-ValSerGluGlyGluAspLeuVals 300
Db 1973 TACTCGTAAATCTTCTGCTCCCGAGGGTCCAGTTATCATGSGGGAAGATGATGTTGTTTC 2032
Qy 300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
Db 2033 CCATGTGGAGGAGTGCATTGTATGATGCTCTAAAAGAA---ATCTTTAAAGTGTGTGTTCCCA 2089
Qy 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys-----336
Db 2090 TAGGTAGCCCTCTCTGTGTGGACTCTGCAGACATCGACCTTTACTCTTCAAAGTAGATCCC 2149

Qy 336 -----336
Db 2150 AACTTTGATGCTATCCCATGACATTTTAAGACATCTTTGAAATGATCATATAAATATT 2209
Qy 336 -----336
Db 2210 GTGCTTCATCCATTTGTTTATTTGGAATACATATGAGAACCGTTGNAATGTGAAAGTGG 2269
Qy 336 -----336
Db 2270 TGTATTGATTAGAAAAAATAGCTTACTGATAGTTGAATGTTTCCAAAGAAAAAGTAT 2329
Qy 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 2330 TTTATATCTTCTATTTGGTGCATCGAGTACTGGCTGACATATTGATTACCTGTGGA 2389
Qy 348 lIleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
Db 2390 ATTGCCAAAGGATGTAATATTGTAATAGACAGATCCGCTTCGTGCTTGTCAAGTTT 2449
Qy 368 GlyLeuAsp-----370
Db 2450 GGGCTTGATAGGTATGATACAAGTGATTCGAAAGAGCCCTTTATTTCTCTATTCTTTG 2509
Qy 370 -----370
Db 2510 CTTTTTTGTTTCTGGAAAAACAATTATAGCTCCAAATGTTTCGCAGAAATATTAGGTTGATG 2569
Qy 371 -----ArgLysTyrLeuIleAspLeuIleGlyArgProGly 382
Db 2570 AGTGGAAAAATTTGTTTGGTTTCAGGAGTACCTGTTGATTATTAGTAGGAAGACCCAGGT 2629
Qy 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
Db 2630 CACTTATCGAGCCCTGATTCCTTCTAAATGGTCTCTCACTATCTCAATTTCTCTCT 2689
Qy 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2690 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGACGTGCGATTTTAGGTACTAGCCAAA 2749
Qy 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer-----439
Db 2750 CAATATTTCTCGATAGCCAGTCTCTTAATCTGTTTTCGATCCTGCATCAGGTATTCCC 2809
Qy 439 -----439
Db 2810 ATACAAAAAACCTAAATAATATGTTAACTTTTTCATCTGCTTACATCTCGTTTGTAT 2869
Qy 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2870 TTCCCTTAAAGAGTAACTCTCTATCA-----TTTAGGTTATT-----2908
Qy 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal-----469
Db 2909 ---CTTGATCATGCTCAGTATCTCAGTGTGATGTTAGTAGTCTTAGAATGATTCTATTGTTG 2965
Qy 470 -----ValThrGlyAsp-----473
Db 2966 TTTTCTGTCTCTTTCACTTACTTGTGTTTGGCTGTGATGTGATGTTGTTGGTGG 3025
Qy 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 3026 GTTCTTTGGCTAATGATATTTAAGGTTAAACTGTTAGTCTGCTGTTTCAAG-----3076
Qy 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 3077 -----CTTATGAATCTAGTGCATTTATGTCAGACTTGTCTCTGAGTCTTAAT 3127
Qy 506 rSerVal-----GlnSerThrPropheValGI 515
Db 3128 TTCTTATATCTGCTTGTGTTGAATGTTGTTAGATGATATGGGATTTCTCAATGTTTCATAGG 3187

QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluuAspSerGluuHisLe 534
 Db 3188 CAATATGATAAATCCGGGTGAGAGAATGACGATGG-----CAGAAAATGGT 3235
 QY 534 uLeuAlaLeuSerHisProArgMet----- 542
 Db 3236 GGTGGGTCTTTGCCACCCAGCTGTAATATGCTCCACAGACATGATGCGTGGTCAAAAT 3295
 QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy 559
 Db 3296 CAAATTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAAACAGGCG 3354
 QY 559 sProAsnGluLeuSerLeuGluAspLeuValIleProTrrPThrAspLeuAspLe 579
 Db 3355 AAATAGGAACCTTGACCTTGATGGTGTATGATATGGACATCCCGTGGTGTGATCTTAATAT 3414
 QY 579 uArgGluIleGlyAla----- 585
 Db 3415 AAAAGAAAAGATTGGAGCAGGTAAATATTTTACGGAAAAATTAATGANTCGGTCTAAAAA 3474
 QY 585 ----- 585
 Db 3475 TGCAAGAAATATGAATTTCTTGAGGAAGTGGTTTGCTTTGGACTCTGTTCTCGACAA 3534
 QY 585 ----- 585
 Db 3535 AATAAGAAAAAGTCCACCCATTTTGAGATTACATTTCTCTGTTGGCTTTAAATCTT 3594
 QY 586 -----GlySerPheGlyThrValTyrArgGlyGluT 596
 Db 3595 CCACTCTAATTTGAGCGACTGCTCTTTTCAGGTTCTTTTGGCACTGTCACCGTGTGAGT 3654
 QY 596 rPHisGlySer----- 599
 Db 3655 GCATGGCTCGTGAAGACTTTTTTGTGAGAAATTTACGCAGCTGAATTTTTTTTCGCTCT 3714
 QY 599 ----- 599
 Db 3715 AAAAATTTGGTGTGACTTTTGGATCTGCTGGTGTATTAATAAAGGCAAGTTATGTATA 3774
 QY 599 ----- 599
 Db 3775 TGTGACTCTCGTCTGCAGAAATTAACACGACAAAGGTGTCCTCAATTTAGATGTA 3834
 QY 599 ----- 599
 Db 3835 TATGTGCTCTTATATATAAAATTTTCTCTGCTGTTGAAATTTACAAATTTCTACTAGA 3894
 QY 600 -----AspValAlaVal 604
 Db 3895 AGAATTCATATTTTGATATTGACATAATATTTCTATCAATTTTCAGGATGTTGCTGTGA 3954
 QY 604 YelLeuThrGluGlnAspPheHisProGluuArgValAsnGluPheLeuArgGluVal- 623
 Db 3955 AAATTCCTGAGCAAGACTTCCATCTGCTGACGCGTGTAAATGAGTTCTTAAGAGGT-G 4013
 QY 623 ----- 623
 Db 4014 CACAAATAAATTTCTCTTGATTTTGGTAATGAACTTTGTTGTTATTAATGTTCTCCAATGA 4073
 QY 624 -----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
 Db 4074 TCTGTATTCGCTGTCAGGTGGGATAAATGAACAGCTTCGCCACCCCTAACATTTCTCT 4133
 QY 637 heMetGlyAlaValThrLysProAsnLeuSerIleValThrGluTyrLeuSer--- 655
 Db 4134 TCAATGGGTGGGTCACTCAACTCCAAATTTGTCAATAGTACAGAAATTTTGTG-C-AAGG 4192
 QY 655 ----- 655
 Db 4193 TACAATTAATCTGGATTTGGAAGTTTGATGTACTGAGTGTAGAAATTTTGGCTTAATGA-4252
 QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667

Db 4253 CTCTAATACCATGATTTCTTTCAACAGAGGTAGTTTATATACAGACTTTTGCATAAAAGTG 4312
 QY 667 lyValIysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
 Db 4313 GAGCAAGGAGCAATTAGATGAGACGTCGCTGAGTATGGCTTATGATGTGTATGTT 4372
 QY 683 ----- 683
 Db 4373 TAACTCTTATGTTACATGATGATGATTACTTCTCGATCTTGGTGTGTTCTTCCACATGG 4432
 QY 684 -----AlaIysGlyMetAsnTyrLeuHisArgAspAsp 694
 Db 4433 AACTTTCTTTTCCAAATCTCTGTGCACAGCTAAGGAATGAATATCTTTCACATCGCAAT 4492
 QY 695 ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr 714
 Db 4493 CTTCCAAATTTGTGATAGAGATCTAAATCTCCAAACTTATTGGTTGACAAAATAATACA 4552
 QY 715 ValIysVal----- 717
 Db 4553 GTCAGAGT-TTGAATCTAAATTAGAAATTTGTTGTGTCCAATGTTTGTGATTTTGTATATTT 4611
 QY 717 ----- 717
 Db 4612 ATTCTCTTGTGAGACAGCTTATATATAAATTATGATTTTTTAATTTCTAAATTTGTTGG 4671
 QY 717 ----- 717
 Db 4672 AGACATTTACAAAAGGCTTAATCTGCTGAAACTTTAAAGATACAGAGCCTCAAGCTGT 4731
 QY 717 ----- 717
 Db 4732 CGTCTTAAACAAATCAGAACATTTATTTCTAACTCTCAATTTGTTGTAATTTTCAG 4791
 QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaA-ArgThrPheLeuSerSerLysSerAla 736
 Db 4792 GTTTGTGATTTTGGTCTCTCGGATTTGAAGGCGCAGCAGCTTTCTTTCTCGAAGTCAGCA 4851
 QY 737 AlaGlyThr----- 739
 Db 4852 GCTGGAACCTGATGATTCAGTTTGTGTTGAAACTTAAACACGCTGAACAGAGTAACTTCTT 4911
 QY 740 -----ProGluTrr 742
 Db 4912 CTAGGTCTTATTTCCAATGAAGCTAAATAATTAATGACTTTTGATATATACGCCGAGTG 4971
 QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyr-SerPh 762
 Db 4972 GATGGCACCAGAGTCTCTCGAGATGAGCGCTCTAATGAAAAGTCAGATGTGTACAGCTT 5031
 QY 762 eGlyValIleLeuTrrPgluLeuAlaThrLeuGlnGlnProTrrPyrCysAsnLeuAsnProAl 782
 Db 5032 CGGGTCTATCTTTGGGAGCTTGTCTACATTTGCAACCAACCATGGGGTAACTTAATCCGCG 5091
 QY 782 aGln----- 783
 Db 5092 TCAGGTACTTCCCCTCTAAACATCCCAATAATAATGATTAATTTTGCATTTGGAAGT 5151
 QY 784 -----Va 784
 Db 5152 CCCTCACTCTACATTTTCAATAACATGCTATATATGATCATCCACAAAATGTTTCCATAGT 5211
 QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
 Db 5212 TGTAGCTCGGTTGGTTTCAAGTGTAAACGCGCTGGAGATCCCGGTAACTGATCTCTCA 5271
 QY 804 sLeuAlaSerLeuIleValAlaCysTrrPala----- 814
 Db 5272 GGTTCACCCATATTCGAGGCTTGTGTGAC-CAAGTAGCTTAAAGATTTTCTATCTCTTTT 5330
 QY 815 -----AspGluProTrr 818

QY 289 -----Glyser-ValserGluGlyGluAspLeuVals 300
Db 1973 TACTCGTTAATTCCTGCTTCCCGGGTCCAGTTATCATGCGGGAGACATGAGTTGGTTC 2032
QY 300 erAlaThrLysGluCysSerAspLeuLysGluCysLeuAlaValIleProL 320
Db 2033 CCATGCGGAGAGGAGTCAATGATGGTCTAAAGAA--ATCTTAAAGTGGTTCCTCCA 2089
QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys- 336
Db 2090 TAGTAGCCTCTCTGTGGACCTGACAGACATCGAGCTTTACTCTTCAAGAGTGAATCCC 2149
QY 336 ----- 336
Db 2150 AACTTTGATCTATCCCATGACATTTAAGACATCTTGTGAATGATCATATAAATATT 2209
QY 336 ----- 336
Db 2210 GTGCTTCATCCATTGTTTATTGGAATACATATGAAGACGTTGAATGTGAAAGTGG 2269
QY 336 ----- 336
Db 2270 TGTATTGATTAGAAAAAATAGTTACTGATGATGTTGAATGTCCAAAGAAAAAAGTAT 2329
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 2330 TTTATATCTTCTATTGGTGATGACAGTACTGGCTGACATAATTGAATTTACCTGTGCA 2389
QY 348 IleAlaLysGlyCysLysTyrCysThrArgAspAlaSerSerCysLeuValArgPhe 367
Db 2390 ATTGCCAAGAGATGAATAATTGTAATAGAGAGATGCCCTTCGTGCTGTGAGGTTT 2449
QY 368 GlyLeuAsp----- 370
Db 2450 GGGCTTGATAGTATGATACAGTGTATGCGAAGAGCCTTTATTTCCTATTTCTTTTG 2509
QY 370 ----- 370
Db 2510 CTTTTTGTCTCGAAAAACAATTATAGTCCAAATGTTTCGAGAAATATTAGTTGATG 2569
QY 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
Db 2570 ACGTGGAAATTTGTTTGGTTCAGGGAGTACTGTTGATTTAGTAGGAAGCCAGGT 2629
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerPro 402
Db 2630 CACTTATGGGAGCCTGATTCCTTGTCTAAATGGTCCCTCATCTATCTCAATTTCTCTCT 2689
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2690 CTGGGTTTCCACACACAGCCAGTGTGAACCCGAGTCGATTTTAGTTACTAGCCAAA 2749
QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer----- 439
Db 2750 CAATATTCTCCGATAGCCAGTCTCTTAATCTTGTGTTTCGATCCTGCATCAGGTATTCC 2809
QY 439 ----- 439
Db 2810 ATACAAAAAAGCTAAATAATGTTAACTTTTTCATGCTGCTTACATCTCGTTTGTAT 2869
QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2870 TTCCCTCTAAAGAGTAATCTCCTCA-----TTTAGGGTATTT----- 2908
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
Db 2909 ---CTTGATCATGCTCATGATCTCAAGTGTAGTAGTCTTAGAATGATCTATTGTTG 2965
QY 470 -----ValThrGlyAsp----- 473
Db 2966 TTTTCTGTCTCTTTTCACTTTAGTTGTTTGGCTGTGATGATGTTGTTGGTGG 3025
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486

Db 3026 GTCTTTGCCTAATGATATTAAGTTAAACTTGTAGTCTGCTGTTCAAG----- 3076
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 3077 -----CTATGAATTCATGTCATTTATGTCAGAGACTTGTCTTCTGAGACTCTAAT 3127
QY 506 rSerVal-----GlnSerThrProPheValG1 515
Db 3128 TTTCTATTATCTGCTTGTGTTGATGGTTGTAGATGATGGATTTCTCAATGTTTCATAGG 3187
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 3188 CAATATGATAATCCGGTGGAGAGAAATGACGCAATGG-----CAGAAAAATGGT 3235
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 3236 GGTGGTCTTTGGCCACCCAGCTGCTAAATGTCCTCCACAGACATGATGCGTGGCTCAAT 3295
QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy 559
Db 3296 CAAATTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGC 3354
QY 559 sProAsnGlnLeuSerLeuGlyLeuGluAspLeuValIleProThrThrAspLeuAspLe 579
Db 3355 AAATAGCGGAACCTTGACTTGATGTGATGATGATGATGATGATGATGATGATGATGAT 3414
QY 579 uArgGluLysIleGlyAla----- 585
Db 3415 AAAAGAAAGATTTGGAGCAGGTAATTAATTTACGAAAAATTAATGATTCGGTCTAAAAA 3474
QY 585 ----- 585
Db 3475 TGCAAGAAATATGAATTTCTTGAGGAAGTGTGTTGCTTGGACTCTGTTCTCGAACAA 3534
QY 585 ----- 585
Db 3535 AATAGAAAAAGTCCACCCATTTTGAGATTACATTTCTCTGTTGCCCTTTAATTTCTT 3594
QY 586 -----GlySerPheGlyThrValTyrArgGlyGluT 596
Db 3595 CCACTCTAATTTGAGCGACTGCTCTTTTTCAGGTTCCTTTTGGCACTGTCCACCGTCTGAGT 3654
QY 596 rHiSgLySer----- 599
Db 3655 GGCATGCTCGGTAAAGAACTTTTGTGTCAGAAATTTACGACGCTGAAATTTTTTTCGCTCT 3714
QY 599 ----- 599
Db 3715 AAAAAATTGTTGTGACTTTTGGATCTGCTGGTATTATATAAAGCAAGTATTATTGTATA 3774
QY 599 ----- 599
Db 3775 TGTGACTCTCGGTTCTGTCAGAAATTAACACGGACAAAAGGTGTCCTCATTTTAGATGTA 3834
QY 599 ----- 599
Db 3835 TATGTGCTTTATATCATATAAATTTGTCTTCTGTTTGAATTTTACAAATTCATCACTAGA 3894
QY 600 -----AspValAlaValL 604
Db 3895 AGAATCTTAATTTTGAATATTGTCAGTAATATTCTCTATCAATTCAGGATGTTGCTGTA 3954
QY 604 YsileLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal- 623
Db 3955 AAATTCCTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTCTTTAAGAGAGGT-G 4013
QY 623 ----- 623
Db 4014 CACAAATAAAATTTCTCTGATTTTGGTAATGAACTGTTGTTGTTATTAATGTTCTCAATGA 4073
QY 624 -----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637

4074 TCTTGATTCGCTGTCAGGTGGCATAATGAAACGCTTCGCCACCCCTAACATGTTCTCT 4133
QY
637 heMetGlyValValThrLysProPheLeuSerIleValThrGluTyrLeuSer 655
Db
4134 TCATGGGTGGGTCTCACTCAACTCCAAATTTGTCAATAGTGACAGATATTTGTC-AAGG 4192
QY
655 ----- 655
Db
4193 TACAATTACTTGGATTGGAAAGTTTGATGTACTGAGTGTAGATAATTTTGGCCTATATGA 4252
QY
656 ----- ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db
4253 CTCCTAATACCAGTATCTTCAACACAGAGGTAGTTTATACAGACTTTTGCATATAAGTG 4312
QY
667 lyValLysAsp---lleAspGluThrArgArgileAsnMetAlaPheAspVal 683
Db
4313 GAGCAAGGGAGCAATATAGATGAGAGACGTCGCTGAGTATGGCTTATGATGTGTATGTT 4372
QY
683 ----- 683
Db
4373 TAACTCCTTATGTTACATGATATGGGTGATTAATCTCTGATCTTGGTGTCTTCACATGG 4432
QY
684 ----- AlaLysGlyMetAsnTyrLeuHisArgArgAsp 694
Db
4433 AACTTCTTCTTCCAAATTCCTGTCACAGGCTAAGGGAATGAATATCTTCAATCGCAAT 4492
QY
695 ProProIleValIleArgAspLysSerProAsnLeuValAspLysLysTyrThr 714
Db
4493 CCFCCAAATGTGCATAGAGATCTAAATCTCCAAACTTATTTGGTTGACAAAATATACA 4552
QY
715 ValLysVal----- 717
Db
4553 GTCAAGGT-TTGAATCTAAATTAGAAATTTGTGTGTCCTCAATGTTTGTATTTGATATTT 4611
QY
717 ----- 717
Db
4612 ATTCTCTCTTGTGAGACAAGCTTATATATAAATATATGATTTTAAATCTPAAATGGTTGG 4671
QY
717 ----- 717
Db
4672 AGACATTACAAAAGGCGTTAATCTGCTGAACCTTAAAGATACAGCAGCCTCAAGCTGT 4731
QY
717 ----- 717
Db
4732 CGCTTTAAAACAATCAGAACATTTATTTCACTCTCTCAATTTGCTGAAATTTTCAG 4791
QY
718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db
4792 GTTTGTGATTTTGGTCTCTCGGATTTGAAGGCCACGAGTCTTCTCTCGAAGTCAGCA 4851
QY
737 AlaGlyThr----- 739
Db
4852 GCTGGAACCGTAAGTTTCAGTTTGTGTTGAACTAAACACACGCTGAACACGTAACCTTCTT 4911
QY
740 ----- ProGluThr 742
Db
4912 CTAGGTCTTATTTCCAAATGGAAGCTTAATAATTAATGATATATTTGTCATTTGGAAGT 4971
QY
742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db
4972 GATGGCACCAGGAAGTCTCGGAGATGAGCGCTCTAATGAAAGTCAGATGTGTACAGCTT 5031
QY
762 eGlyValIleLeuTyrGluLeuAlaThrLeuGlnProTTPCysAsnLeuAsnProAl 782
Db
5032 CGGGGTCACTTGTGGGAGCTTGCTACATTTGCAACACCATGGGGTAACCTTAATTCGGC 5091
QY
782 aGln----- 783
Db
5092 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATGATATATTTTGCATTTGGAAGT 5151
QY
784 -----Va 784
Db
5152 CCCTCACTCTACATTTTCATAACATGCTATATATATGATCATCCCAAAAATGTTCATAGGT 5211

QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 5212 TGTAGCTGCGGTGGTTTCAAGTGTAAACGGCTGGAGATCCCGGTAATCTGAATCTCA 5271
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 5272 GGTTCGACCCATAATCAGGGTGTGGAC-CAAGTACGTTAAGATTTTCTATCTTTT 5330
QY 815 ----- AspGluProTr 818
Db 5331 TTGAATTTCTTCTTGAATAGACTTCATGTTTATGTGTGTTTCAATACCACTGAGCCATG 5390
QY 818 pLysArgProSerPheSerSerIleLeuThrLeuLysProMetThrLysGlnAlaPr 838
Db 5391 GAAGCGTCCATCATTTTGCACCTATAATGAGACTTGTCTAAGACCAATTCATCAATCAGCGT 5450
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5451 TCCTCCGCCCAACCGCTCGGAT 5472

RESULT 9

US-08-003-311B-7
; Sequence 7, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-003-311B-7

Alignment Scores:
Pred. No.: 2,79e-202 Length: 6312
Score: 2069.00 Matches: 556
Percent Similarity: 41.83% Conservative: 110
Best Local Similarity: 34.92% Mismatches: 159
Query Match: 46.65% Indels: 772

DB:	1	Gaps:	34
US-09-904-389-2	(1-850) x US-08-003-311B-7	(1-6312)	
Qy	1	MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu	20
Db	776	ATGGAAATGCCGGTTAGAAGATCTAATACATCTTTGCTTAGTCATATTTCTGACGATCAG	835
Qy	21	ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla	35
Db	836	GTGTGATGTTCCGTCAACCGAGCTCTCCGCCCTCACTATGATTCCTTGTCCAGCGAAAAC	895
Qy	36	-----GlyGlyAsnValIleLeuGlyArgThrAspArg--ValPheAsp	49
Db	896	AGGAGCAACATACACAGCGGGAACACCGGGAAGCTAAGCCGAGGAGCGCGATTTGAT	955
Qy	50	TripAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle	65
Db	956	TGGGATCCTAGCGGTGGTGGTGGTATCATAGGTTGAATAATCAACCGAATCGGTT	1015
Qy	66	Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr	83
Db	1016	GGGAATAATATGATGCTTCGTCTTAGGTTTCGAAGGCAATCCAGTGGGAGTAGTTTC	1075
Qy	84	AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn	103
Db	1076	GGTGAGAGCTCTTTGCTGGGGATTATCATGCTACGCTTCT--GCGGCGGCTAAC	1132
Qy	104	GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal-----	118
Db	1133	GAGATCGAATCTGTGTGATTTCCTCAAGATGATGGGTTTAGGCTTGATTTGGTGGTGGT	1192
Qy	119	-----MetLysAlaValGlySerGlyGly---SerSerGlyLys	130
Db	1193	GGAGGAGATTGAGGATACAGATGGCGCGGAGCTCCGCTGGAGGGCTTCATCTGGGAAG	1252
Qy	131	SerTrpAlaGlnInThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu	150
Db	1253	AGCTGGCGGAGCAGACGCGAGGAGTATACAGCTGCAGCTTCGATTTGGCGTTTAAGGCTT	1312
Qy	151	SerSerAsp***ThrCysAlaAspAspProCAsnPheMetAspProIleProAspGluAla	170
Db	1313	TCGTGGGAGGGCTACTTGTGCGCGAGATCCGAACTTCTGGATCTGTACCGGACGAGTCT	1372
Qy	171	AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp-----	187
Db	1373	GCTTTACGACTTCGCCAAGTTCCAGCGAACCCTTTACATCGTTTCTGGTATTGTT	1432
Qy	187	-----MetLysAlaValGlySerGlyGly---SerSerGlyLys	187
Db	1433	CCTGTTAGCTTTGTTCCCAAAATTAATGTAATCGTGGTTATAGAGATATGGTCCCTCTG	1492
Qy	187	-----	187
Db	1493	TTTCCGAAGTTTCAGTTAGATCTCCTTACCAGAAAGTCTATTAGTAGCAAAATAGATATGT	1552
Qy	188	-----ValAsnGlyCysMe	192
Db	1553	TGTTTATAGATACATTGCAGAGTATGATTTTGTGTGCTGCATCAGGTTAATGGCTGCTT	1612
Qy	192	tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa	212
Db	1613	ATCGTACTATGATAAAGTTCTGTATGGGTTTATATGATGAATGGTCTGGATCCCTATAT	1672
Qy	212	lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLys	232
Db	1673	TTGGACCTTATGATPCGACCTGCATGAAAGTGGTGCATCCCTTCAATTGAATCATTAAG	1732
Qy	232	snhrValaspSerSerIleGlySerIleGluValValLeuIleAspArgHisSerAs	252
Db	1733	ACGTGTGATTTCTGGTGTGATCTTCCTGGTGAACCGATCATAGTTGTAGTAGCGTAGTGA	1792
Qy	252	pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysValThrTh	272

Db	1793	TCAGCCTTCAGGAACTTTCACATAGAGTCCACGACATATCTGTAGCTGCATTACCAC	1855
Qy	272	rlysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly	288
Db	1853	AAAAGAGGTGTGTATCAGCTGGCAAGCTTATCGCAATCGTATGGGTTTGTACTCAT	1912
Qy	288	-----	288
Db	1913	ACAATCCTTACTATCCCTTGAACCTATATTTTATATCTTCCTGTGATTTCTCACATG	1972
Qy	289	-----GlySer-ValSerGluGlyGluAspLeuValS	300
Db	1973	TACTCGTTAAATCTTCTTCCCGAGGTCCAGTTATCATGGGGAAGATGAGTGTGTC	2032
Qy	300	erAlaTrpLysGluCysSerAspLeuLysGluCysLeuGlySerAlaValIleProL	320
Db	2033	CCATGTGGAGAGTGCATTGATGCTCTAAAGAA--ATCTTTAAAGTGTGTGTTCCCA	2089
Qy	320	euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys	336
Db	2090	TAGTAGCCTCTCTGTGTGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGAGATCCC	2149
Qy	336	-----	336
Db	2150	AACCTTGATGCTATCCCATGACATTAAGACATCTTGTGAATGATCATATAAATTAT	2209
Qy	336	-----	336
Db	2210	GTGCTTCATCATTGTTTATTGGAATACATATGAAGAAGTTGAATGTGAAAAGTGG	2269
Qy	336	-----	336
Db	2270	TGTTATTGATTAGAAAATAATAGTTTACTGTAGTTGAATGTTCCAAAGAAAAAGTAT	2329
Qy	337	-----ValLeuAlaAspSerIleAspLeuProCysArg	347
Db	2330	TTTATATCTTCTATTTTGGTGATCGCAGGTACTGGGTGACATAAATGATTACCTCTGCGA	2389
Qy	348	IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe	367
Db	2390	ATTGCCAAGAAGTAAATATTGTTATAGACAGATCGCGCTTCGTGCTTGTCCAGTTT	2449
Qy	368	GlyLeuAsp-----	370
Db	2450	GGGCTTGATAGGTATGATACAAGTGATGCGAAAGAGCCCTTTATTTCGTATTTCTTTG	2508
Qy	370	-----	370
Db	2510	CTTTTGTTCGAAAAACAATTATAGCTCCAAATGTTTCGCAGAAATATTAGGTTGATG	2566
Qy	371	-----ArgGluTyrLeuIleAspLeuIleGlyArgProGly	382
Db	2570	ACGTGGAAAAATTTGTTTGTGTTTCGAGGAGTACTCGTTGATTAGTAGGAAGCAGGT	2622
Qy	383	CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerPro	402
Db	2630	CACATTATCGGAGCCCTGATTCTCTGCTAAATGGTCCCTTCATCATCTCAATTTCTCTCT	2688
Qy	403	LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys	422
Db	2690	CTCGGCTTCACGACCAAGACCAGTGAACCCGCGAGTCGATTTTAGTTTACTAGCATAA	274
Qy	423	GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer-----	439
Db	2750	CAATATTTCTCGATAGCCAGTCTTTAACTTTGTTTTCGATCTGCATCAGGTATTCOC	2800
Qy	439	-----	439
Db	2810	ATACAAAAAACCTAAATAATATGTTAACTTTTTCATCTGCTGCCTTACATCTCGTTTGTAT	2861
Qy	440	-----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg	456

Db 2870 TTCCTCTAAAAGAGTAATCTCTCTATCA-----TTTAGGTATTT----- 2908
Qy 457 ProLeuAsnArgLysAspValaspGlyLysThrIleVal----- 469
Db 2909 ---CTTGATCATGTCTCAGTATCTCAGATGCTAGTAGCTCTAGAAATGATTTCTATTGTTG 2965
Qy 470 -----ValThrGlyAsp----- 473
Db 2966 TTTTCTCTGCTCTTTTCACTTTAGTTGTTTGGCTGTGTGATGTATGTTGTTGGTGG 3025
Qy 474 -----LysAspArgAsnSerGlnLeuAsnLysLysAlaAla 486
Db 3026 GTTCTTTGGCTAATGATATTAAAGTTAAACTGTTAGTCTGCTGTTTCAAG----- 3076
Qy 487 GlnLeuAsnThrGlnAspGlyLysSerGlnGlnPheArgSerCysValAlaSerPro-Ty 506
Db 3077 -----CTTATGAATTTAGTGCAATTTATGTGCAAGACTTGTCTCTGGACTCTAAT 3127
Qy 506 rSerVal-----GlnSerThrProPheValGI 515
Db 3128 TTCTTATATCTCTGTTGTTGAATGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG 3187
Qy 515 uasn---ValValProLeuSerHisIleSerHisIleGlySerGluaspSerGluHisLe 534
Db 3188 CAATATGATAATCCGGGTGGAGAGAAATGACGCAATGG-----CAGAAATAGGT 3235
Qy 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 3236 GGTGGGTCTTGGCCACCAGTCTAATATGCTCCACAGAACATGATGCGTGGCTCAAT 3295
Qy 543 -----AspHisValAsnAsnLeuProPheValHisIleGlySerGlnLeuIleArgLy 559
Db 3296 CAAATTTGAAGCAGCACCTATG-AATGCCCCCAATCAGTCAGCCAGTTCCAAACAGGGC 3354
Qy 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProThrAspLeuAspLe 579
Db 3355 AAATGGGAACCTTGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3414
Qy 579 uArgGluLysIleGlyAla----- 585
Db 3415 AAAAGAAAAGATTGGAGCAGGTAATAATTTTACGGAAAAATTAATGATTCGGTCTAAAAA 3474
Qy 585 ----- 585
Db 3475 TGCAAGAAATATGAATTTCTTGAGGAAGTGGTTTGGCTTGGACTCTGTTCTCGAACAA 3534
Qy 585 ----- 585
Db 3535 AATAAGGAAAAAGTGCACCAATTTTGAGATTACATTTCTCTGTTGCCCTTTAATTTCT 3594
Qy 586 -----GlySerPheGlyThrValTyArgGlyGluT 596
Db 3595 CCACCTAATTTGAGCAGCTGCTCTTTCAGTTTCTTTGGCACTGTCCACCGTGTGAGT 3654
Qy 596 rPhisGlySer----- 599
Db 3655 GGCATGCTCGTGAAGAACTTTTGTGTCAGAAATTTACGCACTGAATTTTTCGTCTCT 3714
Qy 599 ----- 599
Db 3715 AAAAATTTGGTGTGACTTTTGGATCTGTTGGTATTTATTAAGGCAAGATTATGTATA 3774
Qy 599 ----- 599
Db 3775 TGTGACTCTCGTCTGTCTCAGAAATTAACACGACAAAAGGTGCCATTTTAGATGTA 3834
Qy 599 ----- 599
Db 3835 TATGTGCTTTTATATCATAAATTTGCTTCTGCTGTTGAAATTTTACAAATTTCTATCTAGA 3894
Qy 600 -----AspValAlaValI 604
Db 3895 AGAATTTCTAATTTTGTATTATTTGAGTAATATTTCTCTATCAATTTTCAGGATGTTGCTGTA 3954

Qy 604 ystIleuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGlu----- 622
Db 3955 AAATTCCTCATGGAGCAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTTAAGAAA-GGTG 4013
Qy 622 ----- 622
Db 4014 CACAAATAAAATTTTCTCTGATTTTGGTAATGAACCTTGTGTATTAAATGTCTCCAATGA 4073
Qy 623 -----ValAlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
Db 4074 TCTTGATTCGCTGTCAGTTGCGATATGAACCCCTTCCACCCCTACATATTGTTCTCT 4133
Qy 637 heMetGlyAlaValThrLysProAsnLeuSerIleValThrGluTyLeuSer----- 655
Db 4134 TCATGGGTGGGTCACTCAACCTCCAAATTTGTCAATAGTAGCAGAAATATTGTC-AAAG 4192
Qy 655 ----- 655
Db 4193 TACAATTACTTGGANTTGGAGGTTTGATGTACTGAGTGTAGAAATTTTGGCCTATTAATGA 4252
Qy 656 -----ArgGlySerLeuTyArgLeuLeuHisLysSerG 667
Db 4253 CTCTAATACCATGATTTCTTTCAAACAGAGGTAGTTTATACAGACTTTTGCATAAAAGTG 4312
Qy 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
Db 4313 GAGCAGGGAGCAATTAGATGAGAGACGTCGCTGAGTAGTGGCTTATGATGTGTATGTT 4372
Qy 683 ----- 683
Db 4373 TAACTCTTATGTACATGTATGGGTGATTACTTCCGATCTTGGTGTCTTTCACATGG 4432
Qy 684 -----AlaLysGlyMetAsnTyArgLeuHisArgAsp 694
Db 4433 AACTTCTTTCCAAATTTCTGTCTCAGCGCTAAGGGAATGAATATCTTCAATTCGCAAT 4492
Qy 695 ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyThr 714
Db 4493 CTTCCAAATTTGTCATGAGATCTAAATCTCCAACTTATTTGTTGACAAAAATATACA 4552
Qy 715 ValLysVal----- 717
Db 4553 GTCAAGGT-TTGAATCTAAATTAGAAATTTGTTGTCTCAATGTTTGTGATTTT 4611
Qy 717 ----- 717
Db 4612 ATTCCTCTTTGAGACAGCTTATATATAATATGATTTTAAATCTTAATTTGGTTGG 4671
Qy 717 ----- 717
Db 4672 AGACATTACAAAAAGCGTTAATCTGCTGAAACTTAAAGATACAGCAGCCTCAAGCTGT 4731
Qy 717 ----- 717
Db 4732 CGTCTTAAAAACAATCAGAACATTTATTCTTAATCTCTCAATTTGTCTTGAATTTTCAG 4791
Qy 718 ---CysAspPheGlyLysSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4792 GTTTGTGATTTTGGTCTCTCGGATTTGAAGCCAGCACGTTTCTTCTCGAAGTCAGCA 4851
Qy 737 AlaGlyThr----- 739
Db 4852 GCTGGAAACCGTAAAGTTCAAGTTGTTGTAACCTAAACACGCTGAACACGTAACCTTCTT 4911
Qy 740 -----ProGluTr 742
Db 4912 CTAGGTCTTATTTCCAAATGGAAGCTAAATAATTAATCTGACTTTTGATATATCAGCCGAGTG 4971
Qy 742 pMetAlaProGluValLeuArgAspGluProSerAsnGlnLysSerAspValTySerPh 762
Db 4972 GATGGCACCAGAAAGTCTGCGGAGATGAGCCGCTTAATGAAAGTCAGATGTGTACAGCTT 5031

QY 762 eglValleLeuTIPGluLeuAlaThrLeuGlnGlnProTIPcysAsnLeuAsnProAl 782
Db 5032 CGGGTCACTTTGGAGCTTGCTACATTGCAACCAACGATGGGTAACTTAATCCGGC 5091
QY 782 agln----- 783
Db 5092 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATATATTATTTGGCAATG 5151
QY 784 -----Va 784
Db 5152 CCTCACTCTACATTTCAACATGCTATATATGATCATCAACCAAAATGTTCCATAGT 5211
QY 784 lValAlaAlaValIGlyPheGlyGlyLeuAspIleProArgAspValAsnProIly 804
Db 5212 TGAGTCTGGGTTGGTTCAAGGTAAACGGCTGGAGATCCCGGTAACTGTAATCTCTCA 5271
QY 804 sLeuAlaSerLeuIleValAlaCysIrpAla----- 814
Db 5272 GGTTCGAGCCATATATCGAGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTT 5330
QY 815 -----AspGluProTr 818
Db 5331 TTGAATCTCTTGAATAGACTTCATGTTTATGATGTTTCAATTACCAAGTACGCCATG 5390
QY 818 pLysArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 5391 GAAGCGTCCATCATTTGCACTATATATGAACTTGCTTAGACCATGATCAATCAGCGGT 5450
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5451 TCCTCCGCCCAACCGCTCGGAT 5472

RESULT 10
US-08-261-432-7
Sequence 7, Application US/08261432
Patent No. 5602322
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSER: No. 5602322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6312 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-261-432-7
Alignment Scores:
Pred. No.: 2,796-202 Length: 6312
Score: 2069.00 Matches: 556
Percent Similarity: 41.83% Conservative: 110
Best Local Similarity: 34.92% Mismatches: 159
Query Match: 46.65% Indels: 772
Gaps: 34
US-09-904-389-2 (1-850) x US-08-261-432-7 (1-6312)
QY 1 MetGluMetProGlyArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 776 ATGGAATATCCCGGTAGAGATCTAAATTACACTTTGCTTAGCAATTTCTGACGATCAG 835
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 836 GTGTCTGTTTCCGTACCGGAGCTCTCCGCTCCTCATGATTCCTTGTGCGAGGAAAC 895
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 896 AGGAGCAACCATACACGCGGAAACCTAAGCGGAGAGAGAGCGGATTTGAT 955
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgile 65
Db 956 TGGATCTTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1015
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 1016 GGAATAATATATGATCTCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 1075
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAla 103
Db 1076 GGTGAGAGCTCTTTGCTGGGATTTATACATGCTTCTCTCTCTCTCTCTCTCTCTCT 1132
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal----- 118
Db 1133 GAGATCGAATCTCTGGATTTCTCAGAGATGATGGGTTTAGGCTTGGATTTGGTGGTGGT 1192
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 1193 GGAGGAGATTGAGGATACAGATCGCGCGGAGCTCCGCTGGAGGCTCTCATCTGGAG 1252
QY 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 1253 AGCTGGGCGCAGCAGCAGGAGAGATATCATGCTGAGCTTGCATTTGCGCTTAAGGCTT 1312
QY 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
Db 1313 TCGTCGGAGGCTACTTGTCCGACGATCCGAATTTCTGATCTCTGACCGACGAGTCT 1372
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
Db 1373 GCTTTACGACTTCGCAAGTTCAGCGGAAACCGTTTCATGCTGTTTCTGGGTATTGTT 1432
QY 187 ----- 187
Db 1433 CCTGTTAAGCTTTGTTTCCCAAAATTTAATGATCGGTTTATAGATATGTTCTCTTG 1492
QY 187 ----- 187
Db 1493 TTTCGAGTTTTCAGTTAGATCTCTTACCAGAAAGTCTATTAGTAGCAATGAGATATGT 1552
QY 188 -----ValAsnGlyCysMe 192
Db 1553 TGTTTAGATACATTCAGAGATGATGTTTGTGCTGCTCATCAGTTAATGGCTGCTT 1612
QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
Db 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212

REFERENCE/DOCKET NUMBER: UPN-1086

TELEPHONE: 215-568-3100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 5890 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-928-464-6

Alignment Scores:

Pred. No.: 3,15e-202 Length: 5890
Score: 2068.00 Matches: 555
Percent Similarity: 41.83% Conservative: 111
Best Local Similarity: 34.86% Mismatches: 159
Query Match: 46.63% Indels: 772
DB: 1 Gaps: 34

US-09-904-389-2 (1-850) x US-07-928-464-6 (1-5890)

```

Qy 1 MetGluMetProGlyArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 354 ATGGAATGCCCGTAGAAGACTAATTACACTTTGCTTAGTCAATTTCTGACGATCAG 413

Qy 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 414 GTGTCAATTCCTCGTACCAGAGCTCTCCGCTCCTACTATGATTCCTGTGCGGGAAC 473

Qy 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 474 AGGAGCAACCAATACACGCGGAACACCGCGGAAGCTAAGCGGAGAGCGGATTTGAT 533

Qy 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 534 TGGATCCTAGCGGTGGTGGTGTGATCATAGTTGAATATCAATCAACCGAATCGGGTT 593

Qy 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerTyr 83
Db 594 GGGAAATATATGATGCTTCCTCGTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTT 653

Qy 84 AspAspSerSerLeuSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 654 GGTGAGAGCTCTTTGTCTGGGGATTTATACATGCGCTACGCTTTCT---GCGCGGCTAAC 710

Qy 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
Db 711 GAGATCGAATCTGTGGATTCTCCTCAAGATGATGGGTTTAGGCTTGGATTGGTGGT 770

Qy 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 771 GGAGGAGATTGGAGATACAGATGGCGCGGAGCTCCGCTGGAGGGTCTTCTCTGGGAAG 830

Qy 131 SerTrpAlaGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 831 AGCTGGCGGAGAGAGAGAGTATACAGTCGACCTTGCCATTTGGCGTTAGGCTT 890

Qy 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProlleProAspGluAla 170
Db 891 TCGTCGGAGGCTACTTGTGCGGACGATCGGAACCTTTCTCGATCCTGTACCGGACGATCT 950

Qy 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
Db 951 GCYTTACGGACTTCGCCAAGTTTCAGCGGAACCGTTTCACATCGTTTCGGGTATTGTT 1010

Qy 187 ----- 187
Db 1011 CCTGTAAAGCTTTGTTCCCAAAATATTGATCGTGGTTATAGAGATATGTCCTCTTG 1070

Qy 187 ----- 187
Db 1071 TTTCCGAAGTTTCAGTTAGATCTCCTTACCAGAAAGCTATTAGTACCAATAGATATGT 1130

```

```

Qy 188 -----ValAsnGlyCysMe 192
Db 1131 TGTTTAGATACATTGCAGAGTATGATTGTTTGTGCTGCATCAGGTAAATGGCTGCTT 1190

Qy 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
Db 1191 ATCGTACTATGATAAAGTTCTCTGATGGTTTATATGATGAATGGTCTGATCCCTATAT 1250

Qy 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeu 232
Db 1251 TTGGACCTTATGCATCGACCTGCATGAAGTGGTCGATCCCTCAATTGAATCATTAAG 1310

Qy 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
Db 1311 AGCTGTTGATTCTCGTGTGATTCTTCGCTTGAAGCATCATAGTTGATAGGCGTAGTGA 1370

Qy 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
Db 1371 TCCAGCCTTCAAGGAACCTTCACATAGAGTCCAGCATATCTTTAGCTGCATTACCAC 1430

Qy 272 rIySGluValAlaAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
Db 1431 AAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCATCGTATGGGTTTGTACTCAT 1490

Qy 288 ----- 288
Db 1491 ACAATCCTTACTATCCCTTTGAACTTATATATTTTATATCTTCTCTGATTTCTCACATTG 1550

Qy 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
Db 1551 TACTCGTTAAATCTTGTCTCCCGAGGGTCCAGTTATCATGCGGGAAGATGAGTTGGTTC 1610

Qy 300 exAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
Db 1611 CCATGTGGAAGGAGTGCAATGATGCTCTAAAGAA---ATCTTTAAAGTGGTGGTCCCA 1667

Qy 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
Db 1668 TAGGTAGCCTCTCTGTGGACTCTGCAGACATCAGCTTTACTCTTCAAAGTGGATGCC 1727

Qy 336 ----- 336
Db 1728 AACTTTGATGCTATCCCATGACATTTTAAGACATCTTGTGAATGATCATATAAATTATT 1787

Qy 336 ----- 336
Db 1788 GTGCTTCATCCATTTGTTTATTGGAATACATATGAAGACGTTGAATGTGAAAAGTGG 1847

Qy 336 ----- 336
Db 1848 TGTATTGATTAGAAAAAATAGGTTTACTGATAGTTGATGTTCCCAAGAAAAAGTAT 1907

Qy 337 -----ValleuAlaAspSerIleAspLeuProCysArg 347
Db 1908 TTTATATCTTCTATTGTTGTCATGCAGGTACTGCTGCATATAATTGATTTACCTGTGCA 1967

Qy 348 lIleAlaLysGlyCysLysTyrCysThrArgAspAlaSerSerCysLeuValArgPhe 367
Db 1968 ATTGCCAAGGATGTAATATTTGTAATAGACGATGCGCTTGTGCTTGTCTCAGGTTT 2027

Qy 368 GlyLeuAsp----- 370
Db 2028 GGGCTTGATAGGTATGATACAAAGTGAATGCGAAGAGCCTTTATTTCTTCTTCTTTG 2087

Qy 370 ----- 370
Db 2088 CTTTGTGTTTCTGGAAAAACAATTAAGTCCAAATGTTTCGCAGATATTAGGTTGATG 2147

Qy 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
Db 2148 ACGTGGAAAAATTTGTTTGGTTTTCAGGGAGTACCTGTTGATTTAGTAGGAAGCCAGGT 2207

```

393	CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerPro	402
2208	CACATTATGGAGCGCTGATTCCTTAAATGTGCCTCATCTATCTCAATTTCTTCTCT	2267
403	LeuArgPheProArgLeuLysProIleGlusThrIleAspPheArgSerLeuAlaLys	422
2268	CTCGGGTTCCACGACCAAAGCAGTTGAACCCGCGAGTCGATTTTAGTTACTAGCCAAA	2327
423	GlnTyrrPheLeuAspSerGlnSerLeuLeuValPheAspGluAlaSer-----	439
2328	CAATATTCTCCGATAGCCAGCTCTTAATCTGTTTTCGATCCTGCATCAGTATCCCC	2387
439	-----	439
2388	ATACAAAAAACCTGMAATAATATGTTAACTTTTTTGTCATGCTGCTTACATCTCGCTTTTGTAT	2447
440	-----SerGlyAsnValSerGlyLysAspAlaAaPheSerValTyrrGlnAsnG	456
2448	TTCGCCCTAAAGAGTAAATCTCTATCA-----TTTAGGTATTT-----	2486
457	ProLeuAsnArgLysAspValAspGlyLysThrIleVal-----	469
2487	---CTTGATCATGCTCAGTATCTGAAGTGTAGTAGTCTAGAATGATTTCTATTGTTG	2543
470	-----ValThrGlyAsp-----	473
2544	TTTTCTTGCTCTTTTCACATTAGTTGTTTTGGCTGTTGATGTGATGTTGTTGGTGG	2603
474	-----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAaLys	486
2604	GTTCTTTCGCTTAATGATATTAAAGGTTAAACTGTTAGTCTGCTGTTCCAAG-----	2654
487	GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty	506
2655	-----CTTAGTAATCTAGTCGATTTATGTCGAAGACTGTCTTCGGACTCTAAT	2705
506	rSerVal-----GlnSerThrPropheValGI	515
2706	TTCTTTATATCTGCTGTTTGAATGGTTGTAGATATAGGGAATCTCAATGTTTCATAGG	2765
515	uAsn--ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe	534
2766	CAATATGATAATCCGGGTGGAGAGATGAGCGATTGG-----CAGAAAAATGGT	2813
534	uLeuAlaLeuSerHisProArgMet-----	542
2814	GGTGGTCTCTTGGCCACCAGTCGCTAATPATGCTCCACAGAAATGATGGTGGCTCAAT	2873
543	-----AsphisValAsnLeuProPheValHisGlySerGlnLeuLileArgLy	559
2874	CAAAATTGAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGC	2932
559	sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLe	579
2933	AAATAGGGAACCTTGACCTTGATGTGATGATATGGACATCCCCTGGTGTGATCTAATAT	2992
579	uArgGluLysIleGlyAla-----	585
2993	AAAAAGAAAGATTGGAGCAGGTAATAATTTACGAAAAAATTAATGATTCGCTCTAAAAA	3052
585	-----	585
3053	TGCAAGAAATATGAANAATCTTGAGGAAGTGTTTTGCTTTGGACTCTGTTCTCGAACAA	3112
585	-----	585
3113	AATAAGAAAAAAGTCCACCCANTTTGAGATTACATTTCTCTGTGCTTTAATCTT	3172
586	-----GlySerPheGlyThrValTyrrArgGlyGluT	596
3173	CCACTCTAATTTGAGGGACTGCTCTTTCAGGTTCCITTGGCACTGTCACCGTGGTAGT,	3232
596	rPhisGlySer-----	599

Db	3233	GGC	ATGGCTCGGTAAGAACTTTTGTGAGAAATTTAGCAGCTGAAATTTTTTTTCGCTCT	3299
Qy	599	-----	-----	599
Db	3293	AAAA	TTTGGTGTGACCTTTTGGATCTGCTTGGTATTATATAAAGGCAAGTTATTGTATA	3352
Qy	599	-----	-----	599
Db	3353	TGT	GACTCTCGTCTCTCAGAAATTAACACGGACAAAGGTGTCCCATTTTAGATGTA	3412
Qy	599	-----	-----	599
Db	3413	TAT	TGTCCTTTATATCATATAAATTTGTCCTGGTTGAAATTTTACAATTTCTATCACTAGA	3472
Qy	600	-----	-----AspValalaValL	604
Db	3473	AGA	ATTCATTTTGTATTATTCAGTAATATCTCTATCAATTTTCAGGATGTTGCTGTGA	3532
Qy	604	yle	LeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgLuuVal-	623
Db	3533	AAAT	CTCATGGACAAGACTTCATCTGTGAGCGGTGAATGAGTCTTAAAGAGAGGT-G	3591
Qy	623	-----	-----	623
Db	3592	CACA	ATAAATTTTCTCTTGATTTTGGTAATGAACCTTTGTTGTTAATGTCCTCAATGA	3651
Qy	624	-----	-----AlaIleMeLySerLeuArgHisProAsnIleValLeuP	637
Db	3652	TCT	GATTCGCTGCAGTTTGGCATTAATGAACGGCTTCGCCACCCCTAACATTTGCTCT	3711
Qy	637	he	MetGlyAlaValThrLySerProAsnLeuSerIleValThrGluTyrlLeuSer	655
Db	3712	TCAT	GGTGGCGGTCACTCAACCTCCAAATTTTGTCAATAGTGACAGAAATATTGTC-AAGG	3770
Qy	655	-----	-----	655
Db	3771	TACA	ATTACTTGGATTTTGAAGTTTTCATGCTACTCAGTGTAGAATTTTGGCCTATAAGA	3830
Qy	656	-----	-----ArgGlySerLeuTyArgLeuLeuHisLySerG	667
Db	3831	CTCT	AATACCAATGATTTCTTTCAACAGAGGTAGTTTATACAGACTTTTGCATAAAGTG	3890
Qy	667	ly	ValLyAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal	683
Db	3891	GAC	CAAGGAGCAATTATGATGAGAGACGTCGCTGAGTATGCTTATCATGCTGATGTT	3950
Qy	683	-----	-----	683
Db	3951	TAAC	TCTTATGTATACATGTATGGGTGATTACTTCTCGATCTTGGTGTTCTTCACATGG	4010
Qy	684	-----	-----AlaLyseGlyMetAsnTyrlLeuHisArgArgAsp	694
Db	4011	AACT	TTCTTCCAAATCTCTGTCTCAGAGCTAAGGGAATGAATATATCTTCACAAATCGCAAT	4070
Qy	695	Pro	ProIleValHisArgAspLeuLySerProAsnLeuLeuValAspLyAluValThr	714
Db	4071	CCT	CCAAATTTGTGCATAGAGATCTAAAATCTCCAAACTTATTGTTGGTACAAAAAATATACA	4130
Qy	715	Val	lyeVal-	717
Db	4131	GTC	AGGT-TTGAATCTAAATAGAAATTTGTTGTCCTCAATGTTTGTATTTTGATATTTT	4189
Qy	717	-----	-----	717
Db	4190	ATT	CTCTTGTGAGACAAGCTTATATATAAATTATGATTTTAAATTTCTAAATGTTTGG	4249
Qy	717	-----	-----	717
Db	4250	AGCA	ATTACAAAAGCGGTTAATCTGCTGAAACTTAAAGATACAGACGCTCAAGCTGT	4309
Qy	717	-----	-----	717

Db 4310 CGTCTTAAACAACTCAGAACATTAATTCTCACTCTCAATTGCTTGAAATTTTCAG 4369
Qy 718 ---CysAspPheGlyLeuSerArgLeuLysAlaAaGThrPheLeuSerSerLysSerAla 736
Db 4370 GTTTGTGAAATTTGGTCTCTCGGATTAAGGCCAGCAGTTCCTCTCTCGAAGTCAGCA 4429
Qy 737 AlaGlyThr----- 739
Db 4430 GCTGGAACCGTAAGTTTCAGTTTGTGTTGAACTAAACACAGCTGAAACAGTAACTTTCTT 4489
Qy 740 -----ProGluTr 742
Db 4490 CTAGGTCCTATTTCGAATGAAGCTAAATAATTACTGACTTTGATATATACGCCGAGTG 4549
Qy 742 pMetAlaProGluValLeuArgAspGluProSerLysGluLysSerAspValTySerPh 762
Db 4550 GATGGCACCAGAGTCTCTCGAGATGAGCGCTCTAATGAAGAAGTCAGATGTGTACAGCTT 4609
Qy 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Db 4610 CGGGGTCATCTTGTGGAGCTTCTACATTTGCAACACCATGGGTAACTTAATCCGGC 4669
Qy 782 agln----- 783
Db 4670 TCAGGTACTTCCCACTTAAACATCCCAATAATAATGATATATTATTGCAATTTGGAAGT 4729
Qy 784 -----Va 784
Db 4730 CCCTCACTTACATTTTCATTAACATGCTATATATGATCATCCAAATATGTTCCATAGT 4789
Qy 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 4790 TGTAGCTGCGTTTGGTTTCAAGTGTAAACCGCTGGAGATCCCGCGTAACTCTGAATCTCTCA 4849
Qy 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 4850 GGTTCGAGCCATAATACGAGGTTGTTGGAC-CAAGTACGTAAAGATTTTCTATCTCTTTT 4908
Qy 815 -----AspGluProTr 818
Db 4909 TTGAATCTTCTTGAATAGACTTCATGTTTATGTTGTTTCATTACCAAGTGAGCCATG 4968
Qy 818 pLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGluAlaPr 838
Db 4969 GAAGGTCATCATTTTGCATATAATGAGCTTGTCTGAAGACCATTTGATCAATCAATCAGCGT 5028
Qy 838 oProGlnGlnSerArgThrAsp 845
Db 5029 TCCCTCCGCCCAACCGCTCGGAT 5050

RESULT 12
PCT-US93-07347-6
Sequence 6, Application PC/TUS9307347
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07347
FILING DATE: 19930805
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-07347-6
Alignment Scores:
Pred. No.: 3,15e-202 Length: 5890
Score: 2068.00 Matches: 555
Percent Similarity: 41.83% Conservative: 111
Best Local Similarity: 34.86% Mismatches: 159
Query Match: 46.63% Indels: 772
DB: 34 Gaps: 34
US-09-904-389-2 (1-850) x PCT-US93-07347-6 (1-5890)
Qy 1 MetGluMetProGlyValArgSerAspTySerLeuLeuSerGlnIleProAspGluGlu 20
Db 354 ATGGAATCCCGGTGAGAGATCTAATACACTTGTCTAGTCAATTTCTGACGATCAG 413
Qy 21 ValGly-----ThrGlyAlaSerThrSerPheTySerSerValAlaAla----- 35
Db 414 GTCTCAGTTTCCGTCACCGGAGCTCTCCGCTCATATGATTCCTTCGAGCGGAAAC 473
Qy 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 474 AGAGCAACCATTAACAGCGGGAACACCGGGAAGAGTAAGCGGAGAGAGCGGATTTGAT 533
Qy 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyArgIle 65
Db 534 TGGGATCTTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 593
Qy 66 Gly---AsnLeuTy---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTy 83
Db 594 GGAATAATATGATGCTTCGCTCTAGGGTTGCAAGCAATCCAGTGGAGTAGTTTC 653
Qy 84 AspAspSerSerLeuSerSerAspTyTyAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 654 GGTGAGAGCTTTTGTCTGGGATTTATACATGCTACGCTTTCT---GCGGCGGCTAAC 710
Qy 104 GluIleAsnAlaLeuGluTyTrileLeuAspAspAspPheArgVal----- 118
Db 711 GAGATCGAATCTCTTGGATTTCTCAAGATGATGGTTTAGCGCTGGATTTGGTGGTGGT 770
Qy 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 771 GGAGGAGATTGAGGATACAGATGCGCGGAGCTCCGCTGGAGGCTTCTCACTCGGAAG 830
Qy 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 831 AGCTGGCGGAGCAGCAGGAGAGAGTTATACAGCTGCAGCTTGCATTGGCGTTAAGGCTT 890
Qy 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
Db 891 TCGTGGAGGCTACTTGTGCGGACGATCCGAACTTCTGATCTCTGATCCGACGAGTCT 950
Qy 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
Db 951 GCTTTAGGACTTCGCCAAGTTCCAGCCGAAACCGTTTCATCGTTTCTGGGTATTGTT 1010
Qy 187 ----- 187

Db 1011 CTTGTTAAGCTTTGTTCCCAAAATTAATGAATCGTGTATAGAGATATGGTCTCTTG 1070
QY 187 ----- 187
Db 1071 TTTCCGAAGTTTCAGTTAGATCTCTTACCAAAAGTCTATTAGTAGCAAAATGAGATATG 1130
QY 188 -----ValAsnGlyCysMe 192
Db 1131 TGTATTAGATACATGACAGATGATGTTGTTGTGTGCTGCATCAGGTTAATGGCTGCTT 1190
QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuLeuHisGlyMetAspProTyrVa 212
Db 1191 ATCGTACTATGATAAAGTTCTCTGATGGTTTATATGATGAATGCTCTGGATCCCTATAT 1250
QY 212 lTpsSerLeuCysThrAsnLeuGlnLysAspGlyArgLysProSerPheGluSerLeuLys 232
Db 1251 TTGACCTTATGATGACGACCTGCATGAAAGTGTGCGATCCCTTCAATTGAATCATTAAG 1310
QY 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuLeuAspArgHisSerAs 252
Db 1311 AGCTGTTGATCTCTGCTGTTGATCTTCGCTTGAAGCGATCATAGTTGATGAGCGTAGTGA 1370
QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysValThrTh 272
Db 1371 TCCAGCCTTCAGGAACCTTCATATAGAGTCCAGCATATCTGTAGCTGCATTAACAC 1430
QY 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly 288
Db 1431 AAAAGAGGTTTGTGATCAGCTGGCAAGCTTATCTGCAATCGTATGGGTTGTACTCAT 1490
QY 288 ----- 288
Db 1491 ACAATCCTTACTATCCCTTTGAATTAATATTTTATATCTCTCTGATTTCTCACATG 1550
QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
Db 1551 TACTCGTTAACTTCGCTTCCCGAGGGTCCAGTTATCATCGGGGAAGATGAGTTGGTTC 1610
QY 300 eAlaTTPlyGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
Db 1611 CCATCTGGAAGAGTGCATTCATGCTCTAAAGAA---ATCTTAAAGTGGTGGTCCCA 1667
QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys 336
Db 1668 TAGGTAGCTCTCTGTGGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGCAGATCC 1727
QY 336 ----- 336
Db 1728 AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAATTA 1787
QY 336 ----- 336
Db 1788 GTGCTTCATCCATTGTTTATTTGGAATACATATAGAGACGTTGAATGTGAAAGTGG 1847
QY 336 ----- 336
Db 1848 TGTATTGATTAGAAAAAATAGTTACTGATAGTGAATGTTCCAAAGAAAAAGTAT 1907
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 1908 TTTATATCTTCTATTGTTGGTCATGACGAGTACTGGCTGACATAATGATTACCTGTCGA 1967
QY 348 ileAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
Db 1968 ATTGCCAAAGAGTGTAAATATTGTAATAGAGACGATCGCTTCGTGCTTGTGAGTTT 2027
QY 368 GlyLeuAsp----- 370
Db 2028 GGGCTTGATAGGTATGATACAGTGTTCGGAAGAGCCTTTATTTTCTTATTTCTTTG 2087
QY 370 ----- 370

2088 CTTTGTGTTTCTCGAAAAACAATATATAGCTCCAAATGTTTCGCAGAAATATAGTTGATG 2147
QY 371 -----ArgLysTyrLeuLeuAspLeuLeuLeuArgProGly 382
Db 2148 ACGTCGAAAAATTTGTTTGGTTTCAGGGAGTACTGTTGTTGATTAGTAGGAAAGCCAGGT 2207
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerSerPro 402
Db 2208 CACTTATCGGAGCTGATCTCTGCTAAATGGTCCCTTCACTATCTCAATTTCTTCTCT 2267
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2268 CTGCGGTTTCCAGCAACCAAGCCAGTGAACCCAGTCGATTTTAGGTTACTAGCCAAA 2327
QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer 439
Db 2328 CAATATTTCTCGATAGCCAGCTCTTAATCTTGTTCGATCTGCATCAGGTATTCCC 2387
QY 439 ----- 439
Db 2388 ATACAAAAACCTGAATAATATGTTAACTTTTTCATGCTGCTTACATCTCGTTTGTAT 2447
QY 440 -----SerGlyAsnValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2448 TTCCCTTAAAGAGTAATCTCTCTATCA-----TTTAGGTAATTT 2486
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal 469
Db 2487 ---CTTGATCATGCTCAGTATCTGAGTGTAGTGTAGTGTAGTGTAGTGTATTTGTTG 2543
QY 470 -----ValThrGlyAsp----- 473
Db 2544 TTTTCTTGTCTCTTTTCACTTTAGTTTGTGTTGGCTGTGTGATGTGTGTTGTTGGTGG 2603
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 2604 GTTCTTTGCCATAATGATATTTAAGGTTAACTGTTAGTCTGCTGTTCAAG----- 2654
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaLaserPro-Ty 506
Db 2655 -----CTTATGAATCTAGTGCATTTATGTGCAAGACTTGTCTTCTGGACTCTAAT 2705
QY 506 rSerVal-----GlnSerThrProPheValG1 515
Db 2706 TTTCTATATCTGCTTGTGTAATGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG 2765
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 2766 CAATATGATAATCCGGTGGAGAGAAATGACGCAATTGG-----CAGAAAAATGGT 2813
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 2814 GGTGGGCTTTTGCACCACCTGCTATATATGCTCCACAGAAACATGATGCGTGGTCAAT 2873
QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuLeuArgly 559
Db 2874 CAATTTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCTCAACAGGCG 2932
QY 559 sProAsnGlnLeuSerLeuGlyLeuGluAspLeuValIleProTyrThrAspLeuAspLe 579
Db 2933 AAATAGGGAACCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2992
QY 579 uArgGluLysIleGlyAla----- 585
Db 2993 AAAGAAAAAGATTGAGCAGGTAATAATTTTACGAAAAAATTAATGATTCGGTCTAAAAA 3052
QY 585 ----- 585
Db 3053 TGCAAAAGAAATATGAAATCTTGTAGGAAGTGGTTTTCCTTTGGACTCTGTTCTCGAACAA 3112
QY 585 ----- 585
Db 3113 AATAAGGAAAAAGTCCACCCATTTTGAGATTACATTTCTTCTGTTGCTTAAATTTCTT 3172

586 QY -----GlySerPheGlyThrValtyrArgGlyGluT 596
3173 Db CCACCTCTAATTGAGCGACTGCTCTTTTCAGGCTCTCTTTGGCAGCTGTCCACCGTCTGAGT 3232
596 QY rPhisGlySer----- 599
3233 Db GGCATGGCTCGGTAAAGAACTTTTGTGCAGAAATTACGCAGCTGAATTTTTTTCGCTCT 3292
599 QY ----- 599
3293 Db AAAAATTTGGTGTGCACCTTTTGGATCTGCTGGTATTATATAAAGGCAAGTATTGTATA 3352
599 QY ----- 599
3353 Db TGTGACTCTCGTCTCTGTGAGAAATTAAACACGACAAAGGTGTCCCAATTTTAGATGA 3412
599 QY ----- 599
3413 Db TATGTGCTTTTATATACATAAATTTGCTCTCTGTTGAAATTTTACAAATTTCTATCACTAGA 3472
600 QY -----AspValalaval 604
3473 Db AGAATTTCTAATTTTGAATTTTACGTAATTTCTCTATCAATTTTCAGGATTTTCTGTGA 3532
604 QY ysileLeuThrGluGlnaspPheHisProGluArgValAsnGluPheLeuArgGluVal - 623
3533 Db AAATTTCTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTCTTTAAGAGAGGT-G 3591
623 QY ----- 623
3592 Db CACAAATAAAATTTTCTCTGTTGTTGTAATGAACCTTTGTTGTAATGATGCTCCAATGA 3651
624 QY -----AlaileMetLysSerLeuArgHisProAsnileValLeuP 637
3652 Db TCTTGTATCGTGTGAGTGGGATTAATGAACGCTTCGCCACCCCTCAACATTTGCTCT 3711
637 QY heMetGlyAlaValThrLysProAsnLeuSerileValThrGluThrLeuSer----- 655
3712 Db TCATGGTGGGTCACTCAACCTCCAAATTTGTCAATAGTGACAGAAATATTGTG-C-AAGG 3770
655 QY ----- 655
3771 Db TACAATTAATTTGGAATTTGAAGTTTGAATGATGAGTGTAGAATTTTGGCCTATATGA 3830
656 QY -----ArgGlySerLeuThrArgLeuLeuHisLysSerG 667
3831 Db CTCTAATACCATGATTTCTTCAACACAGAGGTAGTTTATACAGACTTTTTCATAAAGTG 3890
667 QY lyValLysasp-----lleAspGluThrArgArgileAsnMetAlapheaspVal----- 683
3891 Db GAGCAAGGGAGCAATTAGATGAGAGACGTGCGCTGATGATGCTTATGATGTTGTTGTT 3950
683 QY ----- 683
3951 Db TAACTCCTTATGTATCATGTATGGGTGATTAATCTCTGATCTTGGTGTCTTTCACATGG 4010
684 QY -----AlaLysGlyMetAsnThrLeuHisArgArgasp 694
4011 Db AACTTTCTTTTCCAAATTTCTGTGCACAGGCTAAGGGAATGAATTAATCTTCAATCGCAAT 4070
695 QY ProProfileValHisArgaspLeuLysSerProAsnLeuValAspLysLysThr 714
4071 Db CTTCCTAATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4130
715 QY ValLysVal----- 717
4131 Db GTCAAGGT-TTGAATCTAAATTAGAAATTTGTTGTGTTCAATGTTTGTGATTTTGTATATTTT 4189
717 QY ----- 717
4190 Db ATTCCCTCTGTGAGACAGCTTATATATAAATATGATTTTAAATCTTAAATTTGTTGG 4249

717 QY ----- 717
4250 Db AGACATTACAAAAGCGGTTAATCTCTGAAACTTAAAGATACAGCAGCCTCAAGCTGT 4309
717 QY ----- 717
4310 Db CGTCTTAAACAAATCAGAACATTATTATTCTAACTCTCTCAATTTGTTGAAATTTTCAG 4369
718 QY ---CysaspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
4370 Db GTTTGTGAATTTGGTCTCTCGGATTAAGGCCAGCAGCTTTCTTCTCGAAGTCAACA 4429
737 QY AlaGlyThr----- 739
4430 Db CTGGAACCGTAAAGTTCAGTTTGTGTTGAAACTAAACACGCTGAACACGTAATTTCTT 4489
740 QY -----ProGluTr 742
4490 Db CTAGTCTCTATTTTCCAATGGAAGCTAAATAATTAATTAATTAATTAATTAATTAATTAAT 4549
742 QY pMetAlaProGluValLeuArgaspGluProSerAsnGluLysSerAspValtyrSerPh 762
4550 Db GATGCCACCAAGTCTCTGAGATGAGCGCTCTAATGAAAGTCTAGATGTTGACAGCTT 4609
762 QY edlyValrileLeuTrpGluLeuAlaThrLeuGlnProTrpCysAsnLeuAsnProAl 782
4610 Db CGGGTCTATCTTGTGGAGCTTGTCTACATTGCAACCAACCATGGGGTAACTTAAATCCGGC 4669
782 QY agln----- 783
4670 Db TCAGTACTTCCCCTCTAAACATCCCAATATAATATATATATTTTGCATTTGGAAGT 4729
784 QY -----Va 784
4730 Db CCCTCACTCTACATTTTCATAACATGCTATATATATATATATATATATATATATATATAT 4789
784 QY lvalalalavalGlyPheLysArgLeuAspPheProArgaspValAsnProLy 804
4790 Db TGTACTCGGTGTGTTTCAAGTGTAAACGCTGGAGATCCCGGTAAATCTGAATCTCTCA 4849
804 QY sleuAlaSerLeuileValAlaCysTrpAla----- 814
4850 Db GTTGCAGCCATTAATCGAGGTGTGTGGAC-CAAGTACGTAAAGATTTTCTATCTCTTT 4908
815 QY -----AspGluProTr 818
4909 Db TTGAATTTCTTGAATAGACTTTCATGTTTATGTTATGTTTATGTTTATGTTTATGTTTATGTT 4968
818 QY pLysArgProSerPheSerSerileMetGluThrLeuLysProMetThrLysGlnAlaPr 838
4969 Db GAAGGTTCATCATTTGCACTATAATGAGCTTCTTAAGACCATTTGATCAAAATCAGCGGT 5028
838 QY oProGlnGlnSerArgThrAsp 845
5029 Db TCCTCGGCCCAACCGCTCGGAT 5050
RESULT 13
US-08-003-311B-6
; Sequence 6, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5444166ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.

	Alignment Scores:		
Pred. No.:	3.54e-202	Length:	6312
Score:	2069.00	Matches:	555
Percent Similarity:	41.83%	Conservative:	111
Best Local Similarity:	34.86%	Mismatches:	159
Query Match:	46.63%	Indels:	772
DB:	1	Gaps:	34
US-09-904-389-2 (1-850)	x US-08-003-311B-6 (1-6312)		

[illegible]

QY	104	GlurleAsnAlaLeuGluTyrIleLeuAepAspPheArgVal-----	118
Db	1133	AGATCGAAATCTGTGTGGATTCTCCATGATGATGGCTTTAGGCTTGGATTGGTGGTGGT 1192	
QY	119	-----MetLysAlaValAlGlySerGlyGly---SerSerGlyLys 130	
Db	1193	GGAGGAGNTTGGAGTACAGATGGCGGGGACTCCGCTGGAGGGTCTTCATCTGGGAG 1252	
QY	131	SerTrpAlaGlnThrGluGluSerPheGlnLeuGlnProLeuValLeuArgLeu 150	
Db	1253	AGCTGGGCGCAGCAGCGAGGAGATTATCAGCTGCAGCTTGCATTTGGCGTTAAAGCTT 1312	
QY	151	SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIlePheAspGluAla 170	
Db	1313	TCGTCGGAGGCTACTTGTGCGGACGATCCGAACCTTTCGGATCTGTACCGGACGAGTCT 1372	
QY	171	AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187	
Db	1373	GGTTTACGGACTTCGCCAAATTTCAGCGGAAACCGTTTCCATCATGTTCTCGGTATTGTT 1432	
QY	187	----- 187	
Db	1433	CCTGTTAGCTTTGTTCCCAAAATATTGAATCGTGGTTATAGAGATATGGTCCCTTCG 1492	
QY	187	----- 187	
Db	1493	TTTCCGAAATTTCAGTTAGATCTCTTACCAAAGTCTATTAGTAGCAATAGATATGT 1552	
QY	188	-----ValaenglyCysMe 192	
Db	1553	TGTTTAGATACATTGCAGAGTATCATTTGTTTGTGTGTCATCAGGTTAATGCTGCT 1612	
QY	192	eSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212	
Db	1613	ATCGTACTATGATAAAGTCTCTGATGGGTTTATATGATGAATGTCGTGGATCCCTAT 1672	
QY	212	ITrpSerLeuCysThrAsnLeuGlnLeuAspGlyArgIleProSerPheGluSerLeuLy 232	
Db	1673	ITGGACCTTATGCATCGACCTGCATGAAAGTGGTGCATCCCTTCAATTGAATCATTA 1732	
QY	232	sThrValAspSerSerleGlySerSerleGluValValLeuIleAspArgHisSerAs 252	
Db	1733	AGCTGTTGATTTCTGGTGTGATTTCTTCGCTTGAAGCGATCATAGTGTGATAGCGTAGTGA 1792	
QY	252	pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272	
Db	1793	TCCAGCCTTCAAGGAACTTCCAAATAGAGTCCAGGACATATCTTGTAGCTGCATTACC 1852	
QY	272	LysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288	
Db	1853	AAAAGAGGTTGTGATCAGCTAGCTGGCAAAGCTTATCTGCAATCGTATGGGTTTGTACTCAT 1912	
QY	288	----- 288	
Db	1913	ACAATCTTACTATCCCTTTGAACTTATATTTTATATCTTCTGTGATTTCTCACATTG 1972	
QY	289	-----GlySer-ValSerGluGlyGluAspAspLeuValS 300	
Db	1973	TACTCGTTAAATTCTTGTCTCCCGAGGGGTCCAGTTATATCATGGGGGAAAGATGATGTTGTC 2032	
QY	300	exAlaTrpLysGluCysSerAspLeuLysGluCysLeuGlySerAlaValIleProL 320	
Db	2033	CCATGTGGAAGGAGTGCAATTCATGGTCTAAAGAA--ATCTTTAAAGTGGTGGTTCCTCCA 2089	
QY	320	euCysSerLeuSerValGlyLeuCysArgHisArgAlaIleuLeuPhe-Lys----- 336	
Db	2090	TAGGTAGCCTCTCTGTTGACTCTGCAGATCGAGCTTTACTTCTTCAAGATGAGATGCC 2149	
QY	336	----- 336	
Db	2150	AACTTTGATGCTATCCCATGACATTTAAGACATCTTTGTGAAATGATCATATAAATATT 2209	

QY	336	-----	336
Db	2210	GTGCTTCATCCATTGTTTTTATTGGAAATACATAAGAACCGTTGAATGTGAAAAAGTGG	2269
QY	336	-----	336
Db	2270	TGTTATTGATTAGAANAANATAGTTTACTGTATGATTGAATGTTCCAAAAGAAAAAAGTAT	2329
QY	337	-----ValLeuAlaAspSerIleAspLeuProCysArg	347
Db	2330	TTTATATCTTCTATTGGTGCAATGCAGGTACTGGCTGACATAAATTGATTATACCCTGTGCA	2389
QY	348	IleAlaLysGlyCysLysTyrcysThrArgAspAspAlaSerSerCysLeuValArgPhe	367
Db	2390	ATTGCCAAGAGTAATAATTGTATATAGACGATCGCGCTTCGTGCGCTTGT CAGGTTT	2449
QY	368	GlyLeuAsp-----	370
Db	2450	GGGCTTGATAGGTATGATACAAAGTAGATTGCGAAAGAGCCCTTTATTTCCTATTTTCTTTG	2509
QY	370	-----	370
Db	2510	CTTTTGGTTCTGGAAAAACAATTATAGCTCCMAATGTTCCGACAATATTAGGTTGATG	2569
QY	371	-----A:gGluTyzrLeuileAspLeuileGlyArgProGly	382
Db	2570	ACGTGGAAAAATTGTTTGGTTTTCAGGAGTACCTGGTTGATTAGTAGGAAGACCAAGT	2629
QY	383	CysLeuCysGlnProAspSerLeuLeuasnGlyProSerSerIleSerIleSerSerPro	402
Db	2630	CACATTATCGGAGCTGATTCTCTGC-AAATGGTCCTCATCTATCTCAATTTCITCTCCT	2689
QY	403	LeuArgPheProArgLeuLysProIleGluSerThriLeaspPheArgSerLeuAlalys	422
Db	2690	CTGCGGTTTCCAGCACCAAGCCAGTGAACCCGCGAGTCGATTTTAGTTACTAGSCCAA	2749
QY	423	GlnTyzrPheLeuAspSerGlnSerLeuasnLeuValPheAspGluAlaSer-----	439
Db	2750	CAATATTCTCCGATAGCCAGTCTCTTAATCTTGTTTTCGATCCTGCATCAGGTATCCC	2809
QY	439	-----	439
Db	2810	ATACAAAAAACCTAAATAATATGTTAACTTTTTCATGCTGCTTACATCTCGTTTGTAT	2869
QY	440	-----SerglyAsnValValserGlyLyAspAlaalaPheSerValtyrGlnArg	456
Db	2870	TTCCCTAAAAGAGTAATCTCCATCA-----TTTAGGAGTATTT-----	2908
QY	457	ProLeuAsnArgLyAspValAspGlyLyseThriLeval-----	469
Db	2909	---CTTGATCATGCTCMAGTATCGAAGCTTGTAGTAGTCTTAGAATGATCTATTGTTTG	2955
QY	470	-----ValThrGlyAsp-----	473
Db	2966	TTTTCTTGTCCTTTTCACTTTAGTCTGTTTGGCTGTTGATGTATGTTTGGTGG	3025
QY	474	-----LyAspArgAsnSerGlnLeuLeuasnlyslsAlaala	486
Db	3026	GTTCTTTGCCTAATGATATTTAAGGTTAAAACCTTTGTAGTCTGCTGTTCAG-----	3076
QY	487	GlnLeuasnThrGlnAspGlyLyseSerGluGlnPheArgSerCysValAlaSerPro-Ty	506
Db	3077	-----CTTATGAATCTAGTGCAATTTATGTGCAAGACTTGCTCTCGACACTAAT	3127
QY	506	rSerVal-----GlnSerThrPropheValGl	515
Db	3128	TTCTTATATCTGCTTTGTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG	3188
QY	515	uasn---ValValProLeuSerHisIleSerHisIleGlySerGluaspsrGluHisIe	534
Db	3188	CAATATGATTAATCCGGTGGAGAGAAATGACCAATGG-----CAGAAAATGGT	3233
QY	534	uLeuAlaLeuSerHisProArgMet-----	542

QY 838 oProGlnGlnSerArgThrAsp 845
 DB 5451 TCCTCCGCCAACCGCTCGAT 5472

RESULT 15

US-07-928-464-5
 ; Sequence 5, Application US/07928464
 ; Patent No. 5367065
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, Joseph R.
 ; APPLICANT: Kieber, Joseph J.
 ; TITLE OF INVENTION: Constitutive Triple Response Gene and
 ; TITLE OF INVENTION: Mutations
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
 ; ADDRESSEE: No. 5367065
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/928,464
 ; FILING DATE: 19920810
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Miller, Suzanne E.
 ; REGISTRATION NUMBER: 32,279
 ; REFERENCE/DOCKET NUMBER: UPN-1086
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5890 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-07-928-464-5

Alignment Scores:
 Pred No.: 1.03e-201 Length: 5890
 Score: 2063.00 Matches: 555
 Percent Similarity: 41.77% Conservative: 110
 Best Local Similarity: 34.86% Mismatches: 160
 Query Match: 46.52% Indels: 772
 DB: 1 Gaps: 34

US-09-904-389-2 (1-850) x US-07-928-464-5 (1-5890)

QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
 DB 354 ATGGAATGCCGGTAGAAGATCTAATTACACTTTCCTTAGTCAATTTCTCAGCATCAG 413
 QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
 DB 414 GTGTGAGTTTCCTCCGCGAGTCTCCGCTCCTCATGATTCCTTGTGAGCGAAGAAC 473
 QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
 DB 474 AGGAGCAACCAATACACCGCGGAAACCGGAAAGCTAAGCGGAGAGCGCGGATTTGAT 533
 QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
 DB 534 TGGGATCTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 593

QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
 DB 594 GGGATAAATATGTATGCTGCTCTAGGTTGCAAGGCAATCCAGTGGGATGATTTTC 653
 QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
 DB 654 GGTGAGAGCTCTTTGTCCTGGGATTTATACATGCTACGCTTTCT---GCGGCGGCTAAC 710
 QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
 DB 711 GAGATCGAATCTGTTGGATTTTCCTCAAGATGATGGGTTTAGGCTTGGATTTGGTGGT 770
 QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
 DB 771 GAGGAGATTTGAGGATACAGATGCGCGGAGCTCCGCTGAGGGTCTTCTCATCTGGGAAG 830
 QY 131 SerTrpAlaGlnGlnThrGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
 DB 831 AGCTGGCGCAGCAGACGAGAGAGATTTATCAGCTGCAGCTTGCATTGGCGTTAAGGCTT 890
 QY 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
 DB 891 TCGTCGAGGCTACTTGTGCGCAGATCCGACCTTTCTGGATCTGTACCGAGAGTCT 950
 QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
 DB 951 GCTTTACGAGACTTCGCCAAGTTCAGCCGAAACCGTTTTCACATCGTTTCTGGGTATTGTT 1010
 QY 187 ----- 187
 DB 1011 CCTGTTAGCTTTGTTTCCCAAAATTATTGATCGTGGTATTAGAGATATGGTCTCTTG 1070
 QY 187 ----- 187
 DB 1071 TTTCCGAGTTTCAGTTAGATCTCCTTACCAGAAAGTCTATTAGTAGCAAAATGAGATATGT 1130
 QY 188 -----ValAsnGlyCysMe 192
 DB 1131 TGTTAGATACATTCAGAGATAGATGTTGTTGCTGCTGCATCAGGTTAATGGTCTCTT 1190
 QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
 DB 1191 ATCGTACTATGATAAAGTTCCTGATGGGTTTATGATGAATGGTCTGGATCCCTATAT 1250
 QY 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeu 232
 DB 1251 TTGGACCTTATGCATCGACCTGCATGAAGGGTGCATCCCTTCAATGAATCAATTAAG 1310
 QY 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
 DB 1311 AGCTGTTGATTTCTGGTGTGATTTCTTCGTTGAAGCGATCATAGTTGATAGCGTAGTGA 1370
 QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
 DB 1371 TCCAGCCTTCAAGGAACCTTCAATAGAGTCCAGACATATCTTGTAGCTGCATTACCAC 1430
 QY 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
 DB 1431 AAAAGAGTTTGTGATCAGCTGCGCAAGCTTATCTGCAATCGTATGGGGTTGTAATCAT 1490
 QY 288 ----- 288
 DB 1491 ACAATCCTTACTATCCTTTGAACCTTATATTTTATATATCTTCCTGTGATTTCTCACATTG 1550
 QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
 DB 1551 TACTCGTTAAATCTTCTTCCCGGGGTCCAGTTATCATCGTATGGGGAGAGATGAGTTGTT 1610
 QY 300 eAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
 DB 1611 CCATGTGGGAAGAGTGATGATGCTCTAAAGAA---ATCTTTAAAGTGGTGGTCCCA 1657
 QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336

```

1668 Db TAGGTAGCTCTCTGTGGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGAGATCCC 1727
336 Qy -----
1728 Db AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAATGATCATATAAATTATT 1787
336 Qy -----
1788 Db GTGCTTCATCCATTGTTTATTGGAAATACATATGAAGAAGCTTGAATGTGAAGAGTGG 1847
336 Qy -----
1848 Db TGTATTGATTAGAAAAAATAGTTACTGATAGTTGAATGTTCCAAAGAAAAAAGTAT 1907
337 Qy -----
1908 Db TTTATATCTTCTATTGTTGGCATGCAGGTACTGCTGACATATGATTTACCTGTCGA 1967
348 Qy IleAlaLysGlyCysAlaTyrCysThrArgAspAlaSerCysLeuValArgPhe 367
1968 Db ATTGCCAAAGGATGTAATATATTGTAATAGACACGATCCGCTTCGTGCTTGTGAGTTT 2027
368 Qy GlyLeuAsp----- 370
2028 Db GGGCTTGATAGTATGATACAAAGTGAATGCGAAGAGCCTTATTTCCTATTTCCTTTG 2087
370 Qy -----
2088 Db CTTTGTGTTCTGGAAAAACAATTATAGCTCCAAATGTTGGCAGAAATATAGTTGATG 2147
371 Qy -----
2148 Db ACGTGGAAAAATTGTTTGGTTTTCAGGAGTACCTGTTGATTTAGTAGGAAGCCAGGT 2207
383 Qy CysLeuCysGlnProAspSerLeuAsnGlyProSerSerIleSerPro 402
2208 Db CACTATGGGAGCGCTGATTCCTTGTGTAATAGTTCCTTCATCTATCTCAATTTCTCTCT 2267
403 Qy LeuArgPheProArgLeuLysProIleuSerThrIleAspPheArgSerLeuAlaLys 422
2268 Db CTSCGGTTTCCATGACCAAAAGCCAGTGAACCCGAGTCGATTTTAGTTACTAGCCAAA 2327
423 Qy GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer- 439
2328 Db CAATAATTTCTCGATAGCAGTCTCTTAATCTTGTGTTTCGATCTCGATCAGGTATTCCT 2387
439 Qy -----
2388 Db ATACAAAAAACCTGAATAATATGTTAACTTTTTCGATGCTGTACATCTCGTTTGAT 2447
440 Qy -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
2448 Db TTCCCTTAAAGAGTAAATCTCTATCA-----TTAGGGTATT----- 2486
457 Qy ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
2487 Db ---CTTGATCATGCTCTCAGTATCTCAAGTGTAGTAGTCTTAGAATGATCTATTGTTG 2543
470 Qy -----ValThrGlyAsp----- 473
2544 Db TTTTCTTGCTCTTTTCACTTTAGTTGTTTGGCTGTGTAGTGAATGTTTGGTGG 2603
474 Qy -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
2604 Db GTTCTTTGGCTAATGATATTTAAGGTAAACTTGTAGTCTGCTGTTCAAG----- 2654
487 Qy GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
2655 Db -----CTTATGATTTCTAGTCAATTTATGTCAGACCTTGCTCTCTGGAAGTCTAAT 2705
506 Qy rSerVal-----GlnSerThrProPheValGln 515

```

```

2706 Db TTCTTATATCTCTGTTTGAATGTTGTAGATGATATGGGANTTCTCAATGTTTCATAGG 2765
515 Qy uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
2766 Db CAATATGATAATCCGGTGGAGAGAAATGACGCAITGG-----CAGAAATAGGT 2813
534 Qy uLeuAlaLeuSerHisProArgMet----- 542
2814 Db GGTGGTCTTTTCCACCACCGCTGCTATATATGCTCCACAGAACATGATGCGTGGTCAAT 2873
543 Qy -----AspHisValAsnAsnLeuProPheValHisIleSerGlnLeuLeuArgLy 559
2874 Db CAAATTGAAGACGACCACTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGC 2932
559 Qy sProAsnGluLeuSerLeuGlyLeuAspLeuValIleProThrArgAspLeuAspLe 579
2933 Db AATAGGAACTTGGACTTGTGTTGATGATATGGACATCCCGTGGTGTGATCTTAATAT 2992
579 Qy uArgGluLysIleGlyAla----- 595
2993 Db AAAAGAAAAGATTGGAGCAGGTAATAATTTTACGGAAAAAATTAATGATTCGGTCAAAA 3052
585 Qy ----- 595
3053 Db TGCAAAGAAATATGAAATCTTGGAGAGTGGTTTGTCTTGGACTCTGTCTTCGAACAA 3112
585 Qy ----- 595
3113 Db AATAAGAAAAAGTCCACCATTTTGGAGATTACATTTCTCTGTGTCCTTTAATCTT 3172
586 Qy -----GlySerPheGlyThrValTyrArgGlyGluT 596
3173 Db CCATCTAATTTGAGCGACTGCTCTTTCAGGTTCTTTGGCACTGTCCACCGTCTGAGT 3232
596 Qy rHisGlySer----- 599
3233 Db GGCATGGCTCGGTAAAGAACTTTTGTGCAGAAATTAACGACGTGAATTTTTCGCTCT 3292
599 Qy ----- 599
3293 Db AAAAATTTGTTGTGACTTTTGGATCTGCTTGGTATTATAAAGGCCAAAGTATTGTATA 3352
599 Qy ----- 599
3353 Db TGAGACTCTCCGTTCTGTGCAGAAATTAACACGCAAAAGGTGCCCATTTAGATGTA 3412
599 Qy ----- 599
3413 Db TATGTCTCTTATATACATAAATTTGCTCTCTGTTTGAATTTTACAAATTCATCACTAGA 3472
600 Qy -----AspValAlaValL 604
3473 Db AGAATTCATAATTTGATTAATTTGCAGTAATATCTCTATCAATTTCAGGATGTTGCTGTGA 3532
604 Qy yIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal- 623
3533 Db AATATCTCATGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCCTTAAGAGAGGT-G 3591
623 Qy ----- 623
3592 Db CACAAATAAAATTTTCTCTGATTTTGTGTAATGAACCTTGTGTATTAATGCTCTCAATGA 3651
624 Qy -----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
3652 Db TCTGTATTCGCTGTGAGGTGGATATGAAGACCCCTTCGCCACCCCTAACATTTGTTCTCT 3711
637 Qy heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer- 655
3712 Db TCAATGCGGTGCTCACTCACTCCAAATTTGTCAATAGTGAAGAAATATTGTC-AAGG 3770
655 Qy ----- 655
3771 Db TACAAATTAATTTGGAAGGTTTGTATGATCTGAGTGTAGAAATTTTGGCCTTAATGA 3830

```


QY 815 -----AspGluProTr 818
Db 4909 TTGAATTCCTTCTTGAATAGACTTCATGTTATGTTATGTTTCTTATTACCAAGTGGCCATG 4968
QY 818 pLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 4969 GAAGCGTCCATCATTTGCAACTATAATGCACTTGTAAAGACCATTTGATCAAAATCAGCGGT 5028
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5029 TCTCCGCCCAACCGCTCGAT 5050

Search completed: October 24, 2003, 03:01:04
Job time : 272 secs

QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db 3831 CTCTAATACCATGATTTCTTCAACAGAGGAGTAGTTTATACAGACTTTTGCATAAAGTG 3890
QY 567 lYValLysAsp---1LeAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
Db 3891 GAGCAAGGGAGCAATTAGATGAGAGACGTCGCTGAGTATGCTTATGATGTTGTTATGTT 3950
QY 683 ----- 683
Db 3951 TAACCTCCTTATGTATACATGATGATGGGTGATTACTTCTGTGATCTTGGTGTTCCTTACATGG 4010
QY 684 -----AlaLysGlyMetAsnTyrLeuHisArgArgAsp 694
Db 4011 AACTTTCTTTCCAAATCTCTGTGCACAGGCTAGGGAATGATTTCTTCCAAATCCCAAT 4070
QY 695 ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr 714
Db 4071 CCTCCAATTGTGCATAGAGATCTAAATCTCCAAACTTATTGTTGACAAAAAATATACA 4130
QY 715 ValLysVal----- 717
Db 4131 GTCAAGGT-TTGAATCTAAATTAGAAATGTTGTGTGTCCTCAATGTTTGGATTTTGATATTTT 4189
QY 717 ----- 717
Db 4190 ATTCTCTCTGTGAGACAAGCTTATATATAATTAATGATTTTAAATTCATAAATGGTTGG 4249
QY 717 ----- 717
Db 4250 AGACATTACAAAAAGCGTTAATCTGCTGAACTTAAAGATACAGCAGCCTCAAGCTGT 4309
QY 717 ----- 717
Db 4310 CGTCTTAAAAACAATCAGAACATTAATTAATCTCACTCCCTCAATTTCTTCTGAAATTCAG 4369
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4370 GTTTGTGATTTTGGTCTCTCGCGATTGAGCCAGCAGCGTTCTTTCTCTCGAAGTCAGCA 4429
QY 737 AlaGlyThr----- 739
Db 4430 GCTGGAACCGTAAGTTCAGTTGTTGTTGAACTAAACACGCTGAAACGTAACCTTTCTT 4489
QY 740 -----ProGluTr 742
Db 4490 CTAGTCTCTATTTCCAATGGAAGCTAAATAATTAATGACTTTGATATATCAGCCCGAGTG 4549
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4550 GATGGCACCAAGTCTCTCGCGATGAGCCGCTCTAATGAAAGTCAGATGTGTACAGCTT 4609
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Db 4610 CGGGGTCACTTTGTGGAGCTTGTACATTGCAACAACCATGGGGTAACCTTAAATCCGGC 4669
QY 782 eGln----- 783
Db 4670 TCAGGTACTTCCCACTTAAACATCCCAATAATTAATGATATTAATTTTGGATTTGGAAGT 4729
QY 784 -----Va 784
Db 4730 CCTCTCACTCTACATTTTCAATCATGCTATATGATCATCCCAACAAAATGTTCCATAGGT 4789
QY 784 lValAlaAlaValGlyPheLysGlyArgLeuAspIleProArgAspValAsnProLy 804
Db 4790 TGTAGCTGGGTGTGTTTCAAGTGTAAACGGCTGGAGATCCCGGTAAATCTGAATCCTCA 4849
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 4850 GGTTGCAGCCATAATCGAGGGTGTGTTGGAC-CAGTACGTTAAGATTTTCTATCTCTTT 4908

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2003, 02:51:03 ; Search time 942 Seconds
(without alignments)
2419.884 Million cell updates/sec

Title: US-09-904-389-2

Perfect score: 4435
Sequence: 1 MEMGRRSDYLLSQIPDEE.....KPMWKQAPQSQRTDRLSYM 850

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO/US0904389/runat_23102003_171711_80/app_query.fasta_1.1031
-DB=Published Applications NA -QWTF=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOFCU=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0904389@cgn_1.1.345@runat_23102003_171711_80
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/2/pubpna/PT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/2/pubpna/PTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	4433	100.0	3286	10 US-09-904-389-1 Sequence 1, Appli

2	2742.5	61.8	2456	12	US-10-171-404A-47	Sequence 47, Appli
3	1538	24.7	2892	10	US-09-938-842A-1073	Sequence 1073, Ap
4	1193	26.9	2661	10	US-09-938-842A-1085	Sequence 1085, Ap
5	806	18.2	2211	10	US-09-938-842A-1577	Sequence 1577, Ap
6	588	13.3	1662	10	US-09-938-842A-1014	Sequence 1014, Ap
7	513	11.6	1638	10	US-09-938-842A-903	Sequence 903, App
8	507	11.4	1063	14	US-10-106-698-2068	Sequence 2068, Ap
9	504.5	11.4	1365	9	US-09-757-982-6	Sequence 6, Appli
10	504.5	11.4	2120	9	US-09-757-982-4	Sequence 4, Appli
11	475.5	10.7	2719	10	US-09-917-800A-1405	Sequence 1405, Ap
12	469.5	10.6	2229	14	US-10-440-341-6	Sequence 6, Appli
13	469.5	10.6	2510	14	US-10-057-550-89	Sequence 89, Appli
14	469.5	10.6	2510	14	US-10-173-225B-67	Sequence 67, Appli
15	466.5	10.5	3435	12	US-10-210-120-86	Sequence 86, Appli
16	466.5	10.5	3454	10	US-09-969-347-226	Sequence 226, App
17	466.5	10.5	3454	14	US-10-171-581-312	Sequence 312, App
18	457.5	10.3	1627	9	US-09-828-313-16	Sequence 16, Appli
19	457.5	10.3	2975	12	US-10-440-341-2	Sequence 2, Appli
20	457.5	10.3	2977	12	US-09-969-347-207	Sequence 207, App
21	457.5	10.3	2977	12	US-10-371-138-1	Sequence 1, Appli
22	457.5	10.3	2977	14	US-10-057-550-25	Sequence 25, Appli
23	457.5	10.3	2977	14	US-10-173-225B-64	Sequence 64, Appli
24	453	10.2	3393	12	US-10-263-480-1	Sequence 1, Appli
25	453	10.2	5527	10	US-09-880-107-3710	Sequence 3710, Ap
26	452	10.2	3840	12	US-10-204-041-3	Sequence 3, Appli
27	450.5	10.2	1428	10	US-09-938-842A-882	Sequence 882, App
28	445.5	10.0	4705	12	US-10-312-918-1	Sequence 1, Appli
29	445.5	10.0	4786	12	US-10-312-918-3	Sequence 3, Appli
30	445	10.0	3428	14	US-10-153-668-435	Sequence 435, App
31	445	10.0	3428	14	US-10-153-668-437	Sequence 437, App
32	444.5	10.0	3365	14	US-10-153-668-323	Sequence 323, App
33	444.5	10.0	2761	12	US-09-814-353-20138	Sequence 20138, A
34	444.5	10.0	6378	12	US-10-352-157-482	Sequence 482, App
35	440	9.9	3558	13	US-10-143-133-1	Sequence 1, Appli
36	438	9.9	3111	13	US-10-014-882-1	Sequence 1, Appli
37	438	9.9	3518	13	US-10-014-882-3	Sequence 3, Appli
38	438	9.9	5549	12	US-10-354-358-23	Sequence 23, Appli
39	432	9.7	2449	14	US-10-320-801-11	Sequence 11, Appli
40	432	9.7	2456	12	US-10-021-660-41	Sequence 41, Appli
41	432	9.7	2456	13	US-10-186-399-1	Sequence 1, Appli
42	432	9.7	2500	9	US-09-977-269-3	Sequence 3, Appli
43	432	9.7	2500	10	US-09-977-260-3	Sequence 3, Appli
44	432	9.7	2500	11	US-09-977-261-3	Sequence 3, Appli
45	430.5	9.7	2604	14	US-10-171-581-317	Sequence 317, App

ALIGNMENTS

RESULT 1
US-09-904-389-1
; Sequence 1, Application US/09904389
; Patent No. US20020129404A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Schuster, Debra K.
; TITLE OF INVENTION: CTRL HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81)...(81)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (593)...(594)

OTHER INFORMATION: n = A,T,C or G
US-09-904-389-1

Alignment Scores:

Pred. No.: 0 Length: 3286
Score: 4433.00 Matches: 850
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.95% Indels: 0
DB: 10 Gaps: 0

US-09-904-389-2 (1-850) x US-09-904-389-1 (1-3286)

Qy 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGlu 20
Db 133 ATGGAATGCTGGACGGAGCTGATTAATCTCTTTTAAGTCAATTCGGACGAGG 192
Qy 21 ValGlyThrGlyAlaSerThrSerPheTyrAspSerValAlaAlaGlyValAsnValile 40
Db 193 GTTGGAAACGGAGCTTCCATCTCTTTTACGACTCCGTAGACGCTGGGGAACGTTATC 252
Qy 41 LysGlyArgThrAspArgValPheAspTyrAspGlySerGlyAspHisArgLeuAsnThr 50
Db 253 AAAGGGAACCGCATAGAGGTTTTCATTTGGGATGGGAGTGGTGATCACAGGTAAACACG 312
Qy 61 GlnAlaTyrArgIleGlyAsnLeuTyrSerTyrIleGlyLeuGlnArgHisSerGly 80
Db 313 CAGCGTATCGATAGGAACCTGTATTCATGATGTTGGTTTACAGAGACATTCAGTGA 372
Qy 81 SerSerTyrAspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnPro 100
Db 373 AGCAGCTACGATGATAGTCTCTCTCTAGTATGTTACTACGCCAGCGGTATCAACCCCT 432
Qy 101 AlaAlaAsnGluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgValMetIys 120
Db 433 CGACCAATAGATCAATGCAATTCATGATGATTCCTCATGATGATTCGAGTGATGA 492
Qy 121 AlaValGlySerGlySerSerGlyIysSerTyrPalaGlnGlnThrGluGluSerPhe 140
Db 493 GCTGTGGAAAGTGGAGTTCCTCTGGAAGAGCTGGGCCCCAGCAGACGGAAGAGCTTT 552
Qy 141 GlnLeuGlnGlnProLeuValLeuArgLeuSerSerAsp**ThrCysAlaAspAspPro 160
Db 553 CAGTTGCGACGACCTTGGTTCTTAGGCTTCTTCAGATGNNACTTGTGCGATGATCCC 612
Qy 161 AsnPheMetAspProIleProAspGluAlaAlaLeuArgSerLeuSerIleSerAlaGlu 180
Db 613 AACTTTATGATCCGATCCAGACGAGGAGCTTAAAGATCGTTATCGATTCAGCTGAG 672
Qy 181 AlaIleSerHisArgPheTyrValAsnGlyCysMetSerTyrLeuGluIysValProAsp 200
Db 673 GCCATCTCGCATCGGTCTTGGGTAAATGGATGCAATGATATTTGGGAAAGTGGCAGAT 732
Qy 201 GlyPheTyrLeuIleHisGlyMetAspProTyrValTyrPheSerLeuCysThrAsnLeuGln 220
Db 733 GGTTTTATCTAATTCATGGGATGGACCATATGATGATGATGATGATGATGATGATGAT 792
Qy 221 GluAspGlyArgIleProSerPheGluSerLeuIysThrValAspSerSerIleGlySer 240
Db 793 GAGGATGGCGATATACCATATTTGAACTCTGAAACAGTTGATTCAGATTCGGTCA 852
Qy 241 SerIleGluValValLeuIleAspArgHisSerAspAlaSerLeuIysGluLeuGlnAsn 260
Db 853 TCATTTGAAGTAGTTTGTATAGATCGGCATAGTATGATGATGATGATGATGATGATGAT 912
Qy 261 ArgValHisAsnIleSerSerCysValThrThrIysGluValAlaAspHisIleAla 280
Db 913 AGGGTGCATAATATTTCTTCCAGTTGTGTAAACCAAAAGAGGTTGCGATCATATAGCA 972
Qy 281 LysLeuValCysAsnHisLeuGlyGlySerValSerGluGlyGluAspLeuValSer 300
Db 973 AACTGGTATGCAATCACATTGGGGGTTTCACTTCTGAGGAGAGATGACTTGGTTTCT 1032

Qy 301 AlaTyrIysGluCysSerAspAspLeuIysGluCysLeuGlySerAlaValIleProLeu 320
Db 1033 GCCTGGAAGGAATGACGAGTACTTAAAGAAATGTTGGATCTGCTGTGATCCCTTA 1092
Qy 321 CysSerLeuSerValGlyIleuCysArgHisArgAlaLeuLeuPheIysValLeuAlaAsp 340
Db 1093 TGCAGCTTATCTGTGGCTTTGTAGACATCGTCTCTTTTATTTCAAGTCCCTAGCTGAT 1152
Qy 341 SerIleAspLeuProCysArgIleAlaIysGlyCysIysTyrCysThrArgAspAspAla 360
Db 1153 TCAATTGATTTACCTGTGCAATTCGCAAGAGTAAATATTGCACTAGAGATGATGCT 1212
Qy 361 SerSerCysLeuValArgPheGlyLeuAspArgGluTyrIleuIleAspLeuIleGlyArg 380
Db 1213 TCATCTTGCCTTTAGCTTCGGGCTTGATAGGAATATCTCATCGATCTGATGGGAGG 1272
Qy 381 ProGlyCysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSer 400
Db 1273 CCAGGTGCTTATGCAACCTGATTCCTTGTCTCAATGCTCCATCATCTCATCTCATTTCT 1332
Qy 401 SerProLeuArgPheProArgLeuIysProIleGluSerThrIleAspPheArgSerIleu 420
Db 1333 TCACCATTCGATTTCCAGACTAAACCTATTGAATCTACCATTTGATTTCCAGTCACTG 1392
Qy 421 AlaIysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSerSer 440
Db 1393 GCCAAACGATTTCTTGGATAGCCATCACTTAATCTTTGATTTGATGAAGCTTCTTCA 1452
Qy 441 GlyAsnValValSerGlyIysAspAlaAlaPheSerValTyrGlnArgProLeuAsnArg 460
Db 1453 GGTAAATGTTGATCTGGGAAGGATGCTGCTCTCCGTCTATCAAGGCCATTAAATAGG 1512
Qy 461 LysAspValAspGlyIysThrIleValValThrGlyAspIysAspArgAsnSerGlnLeu 480
Db 1513 AAGGATGTAGATGGAACCACTAGTGGTTACTGTGTGCAAGGACAGAAATCTCAGTTA 1572
Qy 481 LeuAsnIysIysAlaAlaGlnLeuAsnThrGlnAspGlyIysSerGluGlnPheArgSer 500
Db 1573 TTAATAAATAAGACACCCCACTGAATCTCAAGATGGAAGTCTGAGCAATTTAGATCA 1632
Qy 501 CysValAlaSerProTyrSerValGlnSerThrProPheValGluAsnValProLeu 520
Db 1633 TGTGTTGCTTCTCCATATAGTGTACAGTCCGCCCTTTTGTAGAAATGTAGTCCCTTA 1692
Qy 521 SerHisIleSerHisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisPro 540
Db 1693 AGCCATATCTCACACATTTGGTCTGAGATTCGGAGCATCTCTTAGCATTTGTCTCATCCA 1752
Qy 541 ArgMetAspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgIysPro 560
Db 1753 AGGATGATCATGTTAAACAATTTACCATTTGTTCTAGTGTAGTCACTGATTAAGAACA 1812
Qy 561 AsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTyrThrAspLeuAspLeuArg 580
Db 1813 AATGAGCTTTCCCTTGGCTTAGAGATTTGGTATTCCATGGACAGATCTTGTATTGAGG 1872
Qy 581 GluIysIleGlyAlaGlySerPheGlyThrValTyrArgGlyGluTyrHisGlySerAsp 600
Db 1873 GAGAAATTTGGACGAGGTTCTTTTGGGACTGTATATCGTGGTGAAGTGGCATGGCTGAT 1932
Qy 601 ValAlaValIysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeu 620
Db 1933 GTTGTGTGAAGATCCCTCACAGAACAGACTTCCATCTCTGAACTGTTAATGAGTTCTG 1992
Qy 621 ArgGluValAlaIleMetIysSerLeuArgHisProAsnIleValLeuPheMetGlyAla 640
Db 1993 AGAGAGGTTGCTATCATGAAATCTTTACGACATCTCTAATATTGTACTGTTATTTGGGTCG 2052
Qy 641 ValThrIysProProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyr 660
Db 2053 GTGACCAAGCCACCAAACTTGTCCATTTGTCCCAATATCTATCGAGAGTACTGTTAT 2112
Qy 661 ArgLeuLeuHisIysSerGlyValIysAspIleAspGluThrArgArgIleAsnMetAla 680

Db 2113 AGCGTTTGGCATAAGTCAGGTTGTCAGACACATAGATGAACACAGTCGCAATAAATATGGCT 2172
Qy 681 PheAspValAlaLysGlyMetAsnTyrLeuHisArgArgAspProProIleValHisArg 700
Db 2173 TTGTGATGGCAAGGATGATGATCTACCTCCACAGAGTGATCTCCCAATGTTTCATCGT 2232
Qy 701 AspLeuLysSerProAsnLeuValAspLysLysTyrThrValLysValCysAspPhe 720
Db 2233 GATTTAAATACCCGATCTGTAGTTGACAAAGATATACAGTCAAGGTTTGTGATTTT 2292
Qy 721 GlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrPro 740
Db 2293 GGTCTCTCCGTTTAAAGCAGCCACATCTTCTCATCCCAATCTGCGAGTGGAGACACT 2352
Qy 741 GluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyr 760
Db 2353 GAATGGATGGCACCAGAGTACTACCGCATCAACCATCAATGAAGAGTGCAGATGTTTAC 2412
Qy 761 SerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsn 780
Db 2413 AGCTTTGGAGTGATTTTGGGAGTTGGCACTTTGCAACAGCCATGGTGTATCTTAAC 2472
Qy 781 ProAlaGlnValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAsp 800
Db 2473 CCAGCTCAGGTTGTCGACGCTGTCGATTTAAGGCCAAAGGCTTGACATCCACAGTGAT 2532
Qy 801 ValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArg 820
Db 2533 GTAATCCCAATTTGGCTTCCCTTAATAGTGGCTGCTGGGCGGATGAGCCATGGAACGT 2592
Qy 821 ProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaProProGln 840
Db 2593 CTTCTCTTTCCAGCATATGGAACCTTGAACCAATGACTAAACAGGCCACCTCAA 2652
Qy 841 GlnSerArgThrAspThrLeuSerValMet 850
Db 2653 CAAAGTCGACAGACACCCCTCTCGGTTATG 2682

RESULT 2
US-10-171-404A-47
; Sequence 47, Application US/10171404A
; Publication No. US20030177529A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
; FILE REFERENCE: 16313-0119
; CURRENT APPLICATION NUMBER: US/10/171,404A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/295,680
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-171-404A-47

Alignment Scores:
Pred. No.: 7,68e-284 Length: 2466
Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: 12 Gaps: 14

US-09-904-389-2 (1-850) x US-10-171-404A-47 (1-2466)

Qy 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 1 ATGGAATGCCCGGTAGAAGATCTAATACACTTCTGCTAGTCAATTTCTTGACATCG 60

Qy 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 61 GTGTACGTTTCCGTCACCGGAGCTCCTCCGCTCCTACATATGATTCCTTCGAGCGCAAAAC 120
Qy 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 121 AGGAGCAACCAATAACAGCGGGAACACCGGGAAGCTAAGCGGAGAGAGCGGATTTGAT 180
Qy 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 181 TGGGATCCTAGCGTGGTGGTGGTGCATCATAGATTGAATAATCAACCGAATCGGGT 240
Qy 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 241 CGGATATATATGATGTTCTCTCTAGGGTTCCAAAGCAATCCAGTGGAGTAGTTTC 300
Qy 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 301 GGTGAGAGCTTTTGTCTGGGGATTTATCATCCCTACGCTTTCT---GCGGCGGCTAAC 357
Qy 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal----- 118
Db 358 GAGATCGAATCTGTGGATTCTCTCAGATGATGGGTTTAGGCTTCGATTGGTGGTGT 417
Qy 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 418 GGAGGAGATTTGAGGATACAGATGGCGCGGACTCCGCTGGAGGGTCTTTCATCTGGGAAG 477
Qy 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 478 AGCTGGGCGCAGCAGAGAGGAGATTATCAGCTGCAGCTGCATTCGATTGGCTTAAGCTT 537
Qy 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProfileProAspGluAla 170
Db 538 TCGTCGGAGGCTACTTGTGCGGACGATCCGAACCTTCTGGATCCTGTACCGGACGAGTCT 537
Qy 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190
Db 598 GCTTTACGGACTTCGCCAAGTTTCAGCCGAAACCGCTTTCATCTGTTCTGGGTTAATGGC 657
Qy 191 CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro 210
Db 658 TGCATTATCGTACTATGATAAAGTTCTCTGATGGGTTTATATGATGAATGCTCTGGATCCC 717
Qy 211 TyrValTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer 230
Db 718 TATATTTGGACCTTATGATCGACCTCATGAAAGTGGTCCGATCCCTTCAATGAATCA 777
Qy 231 LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis 250
Db 778 TTAAGAGCTGTGATTCTGGTGGTGGATTCTTCGCTTGAAGCGATCATAGTTGATAGCGT 837
Qy 251 SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysVal 270
Db 838 AGTGATCCAGCGCTTCAAGGAACTTCACAATAGATGCCACACATATCTTGTAGCTGATT 897
Qy 271 ThrThrLysGluValAlaAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySer 290
Db 898 ACCACAAAGAGGTTTGTGATCAGCTGCGCAAGCTTATCTGCAATCGTATGGGGGCTCCA 957
Qy 291 ValSerGluGlyGluAspAspLeuValSerAlaTrpLysGluCysSerAspAspLeuLys 310
Db 958 GTTATCATGGGGAAGATGAGTTGGTTCCCATGTTGGAAGGAGTGCAATTGATGGTCTAAA 1017
Qy 311 GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis 330
Db 1018 GAA---ATCTTTAAAGTGGTGGTTCCTCCCATAGTAGCTCTCTGTTGGACTCTCAGACAT 1074
Qy 331 ArgAlaLeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys 350
Db 1075 CGAGCTTTACTCTTCAAAGTACTGCTGCACATAATTGATTTACCTCTCGAATTGCCAAA 1134
Qy 351 GlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPheGlyLeuAsp 370

```

Db 1135 GGAATGTAATATATGTAATAGACAGATCCCGCTTCGTGCTCTGTACAGTTTGGGCTGTAT 1194
Qy 371 ArgGluTyrLeuLeuAspLeuLeuGlyArgProGlyCysLeuCysGlnProAspSerLeu 390
Db 1195 AGGAGTACTCGTGTGATTTAGTGAAGACGAGTCACTTATGGGAGCCTGATTCCTTG 1254
Qy 391 LeuAsnGlyProSerSerLeuSerLeuSerProLeuArgPheProArgLeuLeuPro 410
Db 1255 CTAATATGGTCCCTCATCTATCTCAATTTCTCTCTCTGGGTTTCCAGCACCAAGCCA 1314
Qy 411 IleGluSerThrIleAspPheArgSerLeuAlaIysGlnTyrPheLeuAspSerGlnSer 430
Db 1315 GTTGAACCCGAGTGTGATTTAGTGTACTAGCCAAACAATATTCTCCGATAGCCAGTCT 1374
Qy 431 LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla 450
Db 1375 CTTAATCTTGTGTTGATCTCTCATCATCAT-----GATATGGCA 1413
Qy 451 PheSerValTyrGluArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal 470
Db 1414 TTCTCAATGTTTCATAGGCAATATGATTAATCCGGTGGAGAGATGACGATTTGGCAGAA 1473
Qy 471 ThrGlyAspLysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThr 490
Db 1474 AATGGTGGT----- 1482
Qy 491 GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
Db 1483 -----GGGTCT 1488
Qy 511 ThrProPheValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAsp 530
Db 1489 TTGCCACCCAGTGTCAATATGCTCCA----- 1515
Qy 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe 550
Db 1516 ---CAGAACATGATGCGTCAATCAATCAATTTAGACGACGACCTATGATGCCCA 1572
Qy 551 ValHisGlySerGlnLeuLeuArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeu 570
Db 1573 ATCAGTCAGCCAGTTCCTCAAAACAGGCAAAATAGGAACTTTGGACTGTGATGATATG 1632
Qy 571 ValIleProTyrThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThr 590
Db 1633 GACATCCCGTGTGTGATCTTATATATATATATATATATATATATATATATATATAT 1692
Qy 591 ValTyrArgGlyGluTyrHisGlySerAspValAlaValLysIleLeuThrGluGlnAsp 610
Db 1693 GTCCACCGTGTGAGTGGCATGCTCGGATGTTGTGTGATAAATCTCATGGAGCAAGAC 1752
Qy 611 PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg 630
Db 1753 TTCCATGCTGAGCGTGTATATGATTTCTTAGAGAGGTTGGATATATGAAACGCTTCC 1812
Qy 631 HisProAsnIleValLeuPheMetGlyAlaValThrLysProAsnLeuSerIleVal 650
Db 1813 CACCCCTAATCATTTGTTCTTCTATGAGGTCGCTCACTCAACCTCCAAATTTGTCAATAGT 1872
Qy 651 ThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAsp 670
Db 1873 ACAGATATTTGCAAGAGTATGTTTATACAGACTTTTGATATATATATATATATATAT 1932
Qy 671 ---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr 689
Db 1933 CAATTAGATGAGAGCGTCCGCTGATGATGCTTATGATGCGGTAAAGGAATGAATATAT 1992
Qy 690 LeuHisArgArgProIleValHisArgAspLeuLysSerProAsnLeuLeuVal 709
Db 1993 CTTTCAATCGCAATCTCTCAATTTGTCATAGATCTATAATCTCCAACTTATTTGTT 2052
Qy 710 AspLysIleTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaAlaGthr 729

```

```

Db 2053 GACAAAAATATACAGTCAAGTTTGTGATTTTGGTCTCTCGCATTTAGAGCCAGCAGC 2112
Qy 730 PheLeuSerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluValLeuArg 749
Db 2113 TTCTTTTCTTCCAAAGTCAGCAGCTGGAACCCCGAGTGGATGGACACAGAAAGTCTCGGA 2172
Qy 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrPheGluLeu 769
Db 2173 GATGAGCCGCTCTAATGAAAGTCAGATGTGTACAGTTCGGGGTCTCTTGTGGAGCTT 2232
Qy 770 AlaThrLeuGlnGlnProTyrCysAsnLeuAsnProIleGlnValValAlaAlaValGly 789
Db 2233 GCTACATTCACAAACCAATGGGGTAACCTAAATCCGCTCAGGTTGTAGTGGGTGGT 2292
Qy 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuLeu 809
Db 2293 TTCAAGTGTAAACGGCTCGAGATCCCGGTAAATCTGAATCTCTCAGGTTGCAGCATAATC 2352
Qy 810 ValAlaCysTyrPheAlaAspGluProTyrLysArgProSerPheSerSerIleMetGluThr 829
Db 2353 GAGGTTGTGTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCACTATAATGGAATTG 2412
Qy 830 LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp 845
Db 2413 CTAAGACCATTCATCAATCAGCGGTTCTCTCCGCCCAACCGCTCGGAT 2460

```

RESULT 3

```

US-09-938-842A-1073
; Sequence 1073, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1073
; LENGTH: 2892
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1073

```

```

Alignment Scores: 2.2e-154 Length: 2892
Score: 1538.00 Matches: 367
Percent Similarity: 54.94% Conservative: 128
Best Local Similarity: 40.73% Mismatches: 253
Query Match: 34.68% Indels: 154
DB: 10 Gaps: 23

```

US-09-904-389-2 (1-850) x US-09-938-842A-1073 (1-2892)

```

Qy 4 ProGlyArgArgSerAspTyr---SerLeuLeuSerGlnIleProAspGluGluValGly 22
Db 398 CCGATGAGAGAGAGAGAGCTTCTGTGTCTTCCGGGTGATCCCGCT-CGCTTCTCGTCT 456
Qy 23 ThrGlyAlaSerThrSerPheTyrAspSerValAlaAlaGlyGlyAsnValIleLysGly 42
Db 457 ACTTCTTCCCGGATCTATCATTTGTCG---GCTAGGACGGTTAATACATACATGACGA 513
Qy 43 ArgThrAspArgValPheAspTrpAspGlySerGlyAspHisArgLeuAsnThrGlnAla 62

```

Db 514 AACATGTATCGAGCTTTGACAGAGAGTTTCGTCTCC---CGAATGTCAGTGAAGC 570
Qy 63 TyrArgIleGlyAsnLeuTyrSerTrpIleGlyLeuGlnArgHisSerSerGlySerSer 82
Db 571 AGCTTCGCTGGAAGCTTCTTC-----TCCGGGACGAGC 603
Qy 83 TyrAspAsp-----SerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnPro 100
Db 604 GTGGACGGGAATTTCTCCAATTTCTCAAGTCATACAGACGCAAGGAAACTTCGACCACC 663
Qy 101 AlaAlaAsnGluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgValMetLys 120
Db 664 ACGCTGTCTCAGTGAACAAAGAGAA-----GAAGAAGTTGAGTTAGGGAA 711
Qy 121 AlaValGlySerGlyCysSerSerGlyLys-----SerTrpAlaGlnThrGluGlu 138
Db 712 -----CAGGGCAAGAGCAAAAGCAAGCTTAGCGCAAGAGTCAAGAGAA 750
Qy 139 SerPheGlnLeuGlnProLeuValLeuArgLeuSerSerAsp***ThrCysAlaAsp 158
Db 751 GGCATATTCTGACGCTCAGCTTCTAAGTGGCTAAGTTCTCAGCA----- 798
Qy 159 AspProAsnPheMetAspProIleProAspGluAlaAlaLeuArgSerLeuSerIle--- 177
Db 799 -----AACCTAGCATGTGAGTCTGTTCATATACAG 828
Qy 178 SerAlaGluAlaIleSerHisArgPheTrpValaAnglyCysMetSerTyrLeuGluLys 197
Db 829 AGCAGAGATCTATCTCCCTACCGTTTGGGTAAGTGGTTGTATTATCATACAGTGACAG 888
Qy 198 ValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrValTrpSerLeuCysThr 217
Db 889 ATATCAGATGGATTTTACAGTATATTAGGAATGGATCCGTATCTTTGGTTGATGTGAAC 948
Qy 218 AsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLysThrValAspSerSer 237
Db 949 AATCTGAGGATGGCAACGAATTCATCTCTTTGTTACTCAAGAGACTGAGCCGAAT 1008
Qy 238 IleGlySerSerIleGluValValLeuIleAspArgHisSerAspAlaSerLeuLysGlu 257
Db 1009 ---GATACATCAATGGAAGTGTTTTGTAGATAGACGTGAGGACTCAGCTTTAAGAA 1065
Qy 258 LeuGlnAsnArgValHisAsnIleSerSerCysValThrThrLysGluValAlaAsp 277
Db 1066 CTGAGGATGAAGGCATCAGCTAGCTATTCTTCTCAGACAACTAGTCTGCTGCTGAG 1125
Qy 278 HisIleAlaLysLeuValCysAsnHisLeuGlyGlySerValSerGluGlyAspAsp 297
Db 1126 AAATTTGGCAGACTTGTTCGGTCTATATGGGGGGGAATTTCCAGGTGGAGCAAGGTAT 1185
Qy 298 LeuValSerAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaVal 317
Db 1186 CTCAGAAACGATGGAACTGTGTCAACAATAGACTCAAGGAATTTCCGAAATGTATCAT 1245
Qy 318 IleProLeuCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPheLysVal 337
Db 1246 CTTCTATAGTGTAGCTTAACATAGGGGCTTTGCCGGCATCGTCCATCTCTATTAGAAA 1305
Qy 338 LeuAlaAspSerIleAspLeuProCysArgIleAlaLysGlyCysLysTyrCysThrArg 357
Db 1306 TTGGCTGATTACATAGTTTACCATGTCCGATAGCTTCGAGGTTCGAGATCTGTAAAGAG 1365
Qy 358 AspAspAlaSerSerCysLeuValArgPheGly-----LeuAspArgGluTyr 373
Db 1366 AGCCACCAATCTCTTCCTCTGTCAGATTGACGATGACAGGAGCTTTCAAGGAATAT 1425
Qy 374 LeuIleAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeuLeuAngly 393
Db 1426 GTAGTTCACTCATCGGGGAACAGGAATGTCCATGATCCGGAATCTCTCTATCAACGGT 1485
Qy 394 ProSerSerIleSerIleSerProLeuArgPheProArgLeuLysProIleGluSer 413
Db 1486 GAAACACAGGTGCAGATTCTCTCACCTCTTCAAAATGAGTCATCTT----- 1530

Qy 414 ThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeu 433
Db 1530 ----- 1530
Qy 434 ValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal 453
Db 1531 -----ACAGAT 1536
Qy 454 TyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAsp 473
Db 1537 TTTTCCAGCGCTTCGTCATAGTACATCTCTCTTGTCAAGACTGTA----- 1581
Qy 474 LysAspArgAsnSerGlnLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly 493
Db 1582 GAGTCAAAAGACTTCAGGCATCTTTCTTGAAACATTCACAGTTCAGGGAGTCAAGGCCAA 1641
Qy 494 LysSerGluGlnPhe----- 498
Db 1642 GTACACAAAGAAATTTGAGTTGCCTGATAACGACGGGACAGTATGTTGTCTCATATTGAT 1701
Qy 499 ArgSerCysValAlaIleAspProTyrSerValGlnSerThrProPheValGluAsnValVal 518
Db 1702 CAACCTCTCTGCAAAAGTATCATCAATGTTTGTGACAGATCTGTTCTTCGAGCTCTA 1761
Qy 519 ProLeuSerHisIleSerHisIleGlySerGluAsp-----Ser 531
Db 1762 CCACCTTGAT---ATACCACAACTTAGTGAAGAAAGATTGCCCCACAAGAAACCTGCAAA 1818
Qy 532 GluHisLeuLeuAlaLeuSerHisPro----- 540
Db 1819 GAAGAAACCGTTCTATTAGAAAGATCCCAACAGCTATGAAGCAGCAAACTTATCAGTTGAA 1878
Qy 541 -----ArgMetAspHisValAsnAsnLeuProPheValHis 552
Db 1879 CCAGAGATAGTAGAGCTGCACACTCGHAAAGATAAAGAGAGTTTACCTGTTGACGCC 1938
Qy 553 GlySerGlnLeuIleArgLysProAsnGlnLeuSerLeuGlyLeuGluAspLeuValIle 572
Db 1939 ATCTCACCTTACTTG-----ACTATTGAACCTTCTTTGGCATCAGATTGGCTGGAGGTC 1992
Qy 573 ProTrpThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThrValTyr 592
Db 1993 TCATGGAATGAATACATATCAAGAGCGTGTGGTCTGTGATCATTGGAACCTGTTTCA 2052
Qy 593 ArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThrGluGlnAspPheHis 612
Db 2053 CGTGTGAGTGGCATGGATCAGATGTTCTGTCAAGATTTTGTCTATTCAAGATTTCCAT 2112
Qy 613 ProGluArgValAsnGluPheLeuArgGlu-----ValAlaIleMetLys 627
Db 2113 GATGACCAATTCAGAAATTTCTCAGAGGATGTAAAGCAGCGGTTGTATATAGAA 2172
Qy 628 SerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeu 647
Db 2173 CGTGTTCGTACCCAAATGTTGTTCTTCTTCATGGTGTGTGACAGACGACCCCGGTTA 2232
Qy 648 SerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGly 667
Db 2233 TCATAATAACAGATATTTCGCAAGGCGAGTCTTTTTCGCTTATCCATAGCCAGCT 2292
Qy 668 ValLysAsp---IleAspGluThrArgArgIleAsnMetalPheAspVal----- 683
Db 2293 TCTGGGAGTTGCTAGATCAGAGGAGGAGGCTACGTATGGCATTTGGATTGTGTGCT 2352
Qy 684 -----AlaLysGlyMetAsnTyrIleuHisArgArgAspProIleValHis 699
Db 2353 ATTCCCATTTATGCCAAGGGGCTCAACTACCTACATGCTCTTAATCTCTCTGTAGTCAT 2412
Qy 700 ArgAspLeuLysSerProAsnLeuValAspLysLysTyrThrValLysValCysAsp 719
Db 2413 TGGGACTGAAATCTCCAAATCTACTGTTGATGAAGACTGCACAGTGAAGGTTTGGAT 2472

QY 720 PheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThr 739
 Db 2473 TTTGGACTTCAAGATTCAAGCAAACTTTTCATACCAATCTGTTGCAGGAACA 2532

QY 740 ProGluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspVal 759
 Db 2533 CCTGAGTGGATGCTCCAGATTCTTAGAGGGGACCGCAACAGAGAATCAGATGTT 2592

QY 760 TyrSerPheGlyValLeuLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779
 Db 2593 TACAGTTTCGGAGTAGTCTTATGGGAGTTGATTACTTTGCAACAGCCCTTGAATGGACTC 2652

QY 780 AsnProAlaGluValValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArg 799
 Db 2653 AGTCTGCTCAGTGGTGGACAGTTCATTCAGAACAGGCGCTTATTAATCTCTCC 2712

QY 800 AspValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLys 819
 Db 2713 AACACCTCTCCGGTCTTGGTATCTCTAATGGAAGCTTCTGGGAGATGAGCGCTCTCAG 2772

QY 820 ArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaProPro 839
 Db 2773 CGGCCAGCATTTGGTAGTAGTAGTGACACATTAAGAGCTACTAAG---TCTCCGGTG 2829

QY 840 Gln 840
 Db 2830 CAG 2832

RESULT 4

US-09-938-842A-1085
 ; Sequence 1085, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPT300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1085
 ; LENGTH: 2661
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1085

Alignment Scores:
 Pred No.: 2,15e-117 Length: 2661
 Score: 1193.00 Matches: 306
 Percent Similarity: 48.12% Conservative: 130
 Best Local Similarity: 33.77% Mismatches: 234
 Query Match: 26.90% Indels: 236
 DB: 10 Gaps: 28

US-09-904-389-2 (1-850) x US-09-938-842A-1085 (1-2661)

QY 78 SerSerGlySerSerTyrAspAspSerSerLeuSerSerAspTyrTyrAla----- 94
 Db 133 ACTAGCCCTAGCCCTGCATCGACTCTTCTCCGCTCTCTCTCTGTTTGTGTAAACGTTCC 192

QY 95 -----ProThrLeuSer-----AsnProAlaAlaAsnGluIleAsnAlaLeuGlu 109
 Db 193 ACGACAATGCCAGACTGGATACATTGAGCCCTGTTGGCCGTGATCTGACGGCTGTGAT 252

QY 110 TyrIleLeuAspAspPheArgValMetLysAlaValGlySerGlyGlySerSerGly 129
 Db 253 GGTGTT-----GATTCAATTGATG----- 273

QY 130 LysSerTrpAlaGlnGlnThrGluLysPheGlnLeuGlnProLeuValLeuArg 149
 Db 274 -----GAGGAGGAGTACCAGTCCAGTTCAGTTAGTATGGCGATCAGC 312

QY 150 LeuSerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGlu 169
 Db 313 GTCTCT-----GATCCTGATCCGAGAGAG 336

QY 170 -----AlaAlaLeuArg-----SerLeuSerIleSerAla--- 179
 Db 337 AATGAGATACAGCTCAGCTTGCCTCCCTAAGAGGATTAGCCTTGGGGTTTCTGCTCCG 396

QY 180 -----GluAlaIleSerHisArgPheTrpValAsnGlyCys 191
 Db 397 GTCACCGAGCTGATTCCGCCGTTGACATTTCTCTCGCTTCGTTATTGG---TCTGGTTGC 453

QY 191 ----- 191
 Db 454 TCGATTAGCAGGGTTTAAGGAATTAGGATCTTGGCTATGCTGCGAGTGTCTCTTCG 513

QY 192 -----MetSerTyrLeuGluLysVal 198
 Db 514 TTGCGAGTATTTCTGAATCCTAATTGTGGACATAAGGTCATTAAATTATGACCAAGAGTC 573

QY 199 ProAspGlyPheTyrLeuIleHisGlyMetAspProTyrValTrpSerLeuCysThrAsn 218
 Db 574 AGCGATGGATTTTACGATGTGTATGGG-----ATTACATCTAAT 612

QY 219 LeuGlnGluAspGlyArgIleProSerPheGluSerLeuLysThrValAspSerSerIle 238
 Db 613 TCTCTTTTCACAGGGAAGATGCCATCTTCTTGTGATCTTCAAGCGATCTCTATTTCAGAT 672

QY 239 GlySerSerIleGluValValLeuIleAspArgHisSerAspAlaSerLeuLysGluLeu 258
 Db 673 AATGTTGATTAGAGTCACTTAGTTAACAGATTGATCTCTGAACTACAAGAGCTA 732

QY 259 GlnAsnArgValHisAsnIleSerSerSerCys-----ValThrThr 272
 Db 733 GAGAGAGAGATATTCGCTTTGGCTTCGGAATGTCAGACTTTTCTCTCTGTCAGGGTGTCA 792

QY 273 LysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySerValSer 292
 Db 793 AGTGATTGACTCAGAAAATTGCCAAATATAGTTCTAGAGCAAAATGGGTGGCCCGTT--- 849

QY 293 GluGlyGluAspLeuValSerAlaTrpLysGluCysSerAspAspLeuLysGluCys 312
 Db 850 GAAATGCTGATGAAGCATTGAGAGGGTGGATGCTTCGGAGCTATGAACATAAGAAATTC 909

QY 313 LeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHisArgAla 332
 Db 910 TTGAACACTACTATTCTTCCACTTGGTCGAGTTAATGTTGTTCTTGCACGACAGCGGT 969

QY 333 LeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLysGlyCys 352
 Db 970 TTGCTTTTCAAGGTCCTTCTGATAGGATTAAATCTCCATGATGCTGCTGTTAAAGGAGT 1029

QY 353 LysTyrCysThrArgAspAspAlaSerSerCysLeuValArg----- 366
 Db 1030 TACTACACTGGAAGTATGATGGGCTGTGAACCTTGAATTAACCTAGATGACAAAGTCTCT 1089

QY 367 -----PheGlyLeuAspArgGluTyrLeuIleAspLeuLeuGlyArgProGlyCysLeu 384
 Db 1090 AATTCGTTCTTCAATGAGTGAATACATATTATTGATTAAATGGGTGCTCCGGGTGCTCTG 1149

QY 385 CysGln-----ProAspSerLeuLeu----- 391
 Db 1150 ATCCCTTCTGAGGTTCCAAGCAGTTTCTTCCAGTTTCTTCCAGTTTCTTCCAGATACACAGATATT 1209

QY 392 ---AsnGlyProSerSerIleSerIleSerSerProLeuArgPheProArgLeuLys--- 409

Db 1210 CCGAGAAATTTGGACTCTTTGGACATTCATCCCGCTACTTGAGAAAGAAATTTGAAACG 1269
QY 410 -----ProIleuSerThrIleAspPheArgSer---LeuAlaLysGlnTyrPhe 425
Db 1270 CCAGCATTTTCAGTTTCGAGGAACAGATTTCTAGATCTGTATGGTAGCAAACTTCTTC 1329
QY 426 LeuAspSerGlnSerLeuAsn----- 432
Db 1330 ACTGGAACACGAGAAACAGACAGATGCTGTTGTAAGAAACATCAACACAGAGAGA 1389
QY 433 -----LeuValPheAspGluAlaSerSerGlyAsnValVal--- 444
Db 1390 TTTGACATGATTTTGGGAAGTTAATGCACTCACAGCAGATATCTGTGAAATATGCCA 1449
QY 445 -----SerGlyLysAspAla----- 449
Db 1450 CCATTTTCTGGAACCGACTTGTGCAGAGAAAGTTAAAGTTAAATGCTCTCAAGTAT 1509
QY 450 AlaPheSerValTyrGlnArgPro----- 457
Db 1510 GTCATTAAGTGCAGCAAGAAACCCCTGAATTTGCGCAGAAATATACATGCTGTGTTAGAA 1569
QY 458 -----LeuAsnA:GlyAspValAspGly 465
Db 1570 AGTGTGTCATCCCTCCCGAGATTGTTTATGATATATTACCCACATTAAGTTGAGGGG 1629
QY 466 LysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeuLeuAsn----- 482
Db 1630 AAGATTTGCTTCAAGAGCTCCGCCAAGAAAGTAGCAATTTCTATGGTTTCTGGTATTTCCA 1689
QY 483 -----LysLysAlaAlaGlnLeu-----AsnThrGlnAspGlyLysSerGlu 496
Db 1690 TGCTACCCAGAAAGTAGCTGACAACTGAGAGATCTGAAAGCAACCCACAGCCGAG 1749
QY 497 GlnPheArgSerCysValAlaSerProTyrSerValGlnSerThrProPheValGluAsn 516
Db 1750 AGTTACCAACATCACTGGAGGTCGATTTCTCAATGAGGAGGAAGCTTTGATTTGATAAT 1809
QY 517 Val-----ValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLeu 534
Db 1810 ACTGTTAAGCTTCTTCATCCGAAATATGAGGTTGGCACTGCTGATGGGGAGTCTGCT 1869
QY 535 LeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPheValHisGlySer 554
Db 1870 GTTTGTGATGTCATGACCAA----- 1890
QY 555 GlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuVal----- 571
Db 1891 -----GGGATTAATCCATTTGCTCGAGAACT 1917
QY 572 -----IleProThrThrAspLeuAspLeuArgGluLysIleGlyAlaGlySer 587
Db 1918 GCAAAGTGGGAAATTTATGTCGGAAGATCTTCAGATTTGGCGAGCGCATTTGTTGTTCA 1977
QY 588 PheGlyThrValTyrArgGlyGluTyrHisGlySerAspValAlaValLysIleLeuThr 607
Db 1978 TATCGAAGTTTATCTGTCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTTCG 2037
QY 608 GluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLys 627
Db 2038 GACCAAGATTTCTCTGCTGTCATGATTCACACAGTTCAAATCTCAATTTGAAATATGTTG 2097
QY 628 SerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeu 647
Db 2098 AGGTTACGCATCCAAACGTTGTTCTTTTCATGGAGCATTTACTCGTCCCCCAATTTTC 2157
QY 648 SerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGly 667
Db 2158 TCCATCTCGACAGAGTTCTTACCCAGGGAGGAGTTGTTGATAGATTACTCCATCGCCGCAAC 2217
QY 668 ValLysAspIleAspGluThrArgArgIleAsnValAlaPheAspValAlaLysGlyMet 687

Db 2218 ---CATCAGCTTGATGAGACAGAGGAATGCCGATGGCTCTTGTATGTCGCAAGGAATG 2274
QY 688 AsnTyrLeuHisArgArgAspProIleValHisArgAspLeuLysSerProAsnLeu 707
Db 2275 AACTACTATACACACCCAGCCAGCTGTTGTGTATCATAGGGAATTTAAATCTCCAAACCTT 2334
QY 708 LeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAla 727
Db 2335 CTTGTTGATAAAATTTGGTTGTGAGGTTTGTGATTTTGGATTGTCGCCCATGAACAC 2394
QY 728 ArgThrPheLeuSerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluVal 747
Db 2395 CACACATATTTGCTCGAAATCAACTGCAGGAACGCTGAGTGGATGGCTCCAGAGTG 2454
QY 748 LeuArgAspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyr 767
Db 2455 TTGAGGAATGAACCGCTAATGAGAAATGTGACGTGTACAGCTTTGGTGTCAATTTGG 2514
QY 768 GluLeuAlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValValAlaAla 787
Db 2515 GAAATAGTACTTTCACGCGCTCCCTCGAAAGGTTTGAACCCGATGCAAGTCTGGAGCT 2574
QY 788 ValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSer 807
Db 2575 GTGGGATTTCCAGAAATCGACGCTTGAATCCAGATGATATCGATCTAACTGTGGCAG 2634
QY 808 LeuIleValAlaCysTyr 813
Db 2635 ATAATCCGTAATGTTGG 2652

RESULT 5
US-09-938-842A-1577
; Sequence 1577, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1577
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1577

Alignment Scores: 5,838-76 Length: 2211
Pred. No.: 806.00 Matches: 170
Score: 59.75% Conservative: 72
Best Local Similarity: 41.98% Mismatches: 135
Query Match: 18.17% Indels: 28
DB: 10 Gaps: 7

US-09-904-389-2 (1-850) x US-09-938-842A-1577 (1-2211)

QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleValThrGlyAspLysAspArg 476
Db 973 CCTATCTTAAGAAACGGTATCAAT---AAGTCAGCATGTGGCAGTGGAGGTAGTCTTAAG 1029
QY 477 AsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGlyLysSerGlu 496

Db 1030 GCTTCTAATGCACTTACCTGACGGCTTTCAGACAAAT---GGCAATGGAAACCCAAA 1086
Qy 497 GlnPheArgSerCysValAlaSerProTyrSerValGlnSerThrProPheValGluLeu 516
Db 1087 AGGGCTGAAGTTAGAAATTTAGATGCTCTATGGAATAGGAGCTGAGGGTTTGATACATAAT 1146
Qy 517 ValValProLeuSerHisIleSerHisIleGlySerGlu-----Asp 530
Db 1147 GGAGATCGCTTTCAGTATATTGGGAACCTGGGACAAAGTAACCTCCAGAGGACTAGAG 1206
Qy 531 SerGluHisLeuLeuAlaSerHisProArgMetAspHisValAsn----- 547
Db 1207 AGTGGTTGGTCTGGCATGCGGGAACAAATAATGCGACCTAAATGGTGAGATAGAA 1266
Qy 548 -----LeuProPheVal-----HisGly 553
Db 1267 GATGCTTGGAACTACCTGCTTAGTGTGATCCCTTGCCTTCTAGGAGTCAACAGCGGT 1326
Qy 554 SerGlnLeu-----IleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuVal 571
Db 1327 AGGCAACAAAGTCTGTCAACCAAGGAATAATAGATTAGTTACTGATTCGTCGTGTGAG 1386
Qy 572 IleProTyrThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThrVal 591
Db 1387 ATACGATGGGAATCTCAACTTGGGAGGAGGTCGGAAGAGGTTCAITTTGCTGCGGTT 1446
Qy 592 TyrArgGlyGluTyrHisIleSerAspValAlaValLysIleLeuThrGluGlnAspPhe 611
Db 1447 CATGCTGGAGTTGGATGGATCGGATGTTCTATTAGGTTTACTTCCGATGGTGTATAC 1506
Qy 612 HisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArgHis 631
Db 1507 AATGCGATGACTTTCAGCGGATGCAAAAGGAGATCAACATTATGAAGAACTGAGACAT 1566
Qy 632 ProAsnIleValLeuPheMetGlyAlaValThrLysProAsnLeuSerIleValThr 651
Db 1567 CGAATGCTACTATTTATGGGACGATGTACAGAGAAATACTGCCATATCATG 1626
Qy 652 GluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAspIle 671
Db 1627 GAATATATCCAGAGGAGTCTCTTCAAAATATCTTCAATATCAATATCAATATG 1683
Qy 672 AspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyrLeuHis 691
Db 1684 GACAGAAACCGCGTTTAAAGATGGCCCTTATGCTAGGGGATGAATATCATCTACAC 1743
Qy 692 ArgArgAspProProIleValHisArgAspLeuLysSerProAsnLeuValAspLys 711
Db 1744 CGCAGAAATCCGCCAATTTGTACATAGACATTTGAATCTTCCATCTACTCGTGGACAAG 1803
Qy 712 LysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeu 731
Db 1804 AACTGGAATGTCAGGTTGGAGACTTTGGGTTATCAAGTGGAGAACCGCACTTCTTG 1863
Qy 732 SerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluValLeuArgAspGlu 751
Db 1864 AGTACTAAATCCGGGAAAGGAACCTCCGAGTGGATGCTCTGAAGTCTCAGAGTGA 1923
Qy 752 ProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrPgluLeuAlaThr 771
Db 1924 CCTTGAATGAGAAGTGTGTGTGCTTGGAGTCACTTATGGGAGCTAATGACT 1983
Qy 772 LeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValAlaAlaValGlyPheLys 791
Db 1984 AGCTTAGTACCATGGGACCGCTTGAACCTCTATTAGGTTGTGGAGTGTGGTTTCATG 2043
Qy 792 GlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIleValAla 811
Db 2044 GATCGACGATTAGACTTACCTGAAGATTAATAATCCCGGATCGCATCATTAATACAGAT 2103
Qy 812 CysTyrAlaAspGluProTyrLysArgProSerPheSerSerIleMetGluThrLeuLys 831
Db 2104 TGTTGGCAAACTGATCCGACAAACGACCGCTGTCGAGGAATTAATTAGTCAGATGATG 2163

Qy 832 ProMetThrLysGln 836
Db 2164 AGCTGTTCGCGAAA 2178

RESULT 6

US-09-938-842A-1014
Sequence 1014, Application US/09938942A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1014
LENGTH: 1662
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1014

Alignment Scores:
Pred. No.: 9,596-53 Length: 1662
Score: 588.00 Matches: 165
Percent Similarity: 51.06% Conservative: 99
Best Local Similarity: 31.91% Mismatches: 174
Query Match: 13.26% Indels: 81
DB: 10 Gaps: 21

US-09-904-389-2 (1-850) x US-09-938-842A-1014 (1-1662)

Qy 346 CysArgIleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuVal 365
Db 201 TCTCCATATGCTTTGGATGATAA---TGTTG-AGAGGACAGAGATGTACTTACTCATC 256
Qy 366 ArgPheGlyLeuAsp-----ArgGluTyrLeuLeuAspLeuIleGlyArg 380
Db 257 AGA-----GATTGTTGAAATTTGGCTGAAGATCTGTACTAGACCTGTTTTCGAAG 307
Qy 381 ProGlyCysLeuCysGlnProAspSerLeuLeuAsnGly-----Pro 394
Db 308 TT-CGTTGTTG----CAGTTTCTCCACATTTGAATGAAATCTGTGTGACGTTGATCCT 363
Qy 395 SerSerIleSerIleSerSerProLeuArgPheProArgLeuLysProIleGluSerThr 414
Db 364 TGGGATCTTCGCGGTCAAT-----GAAGATGCTCAAGAGCTCC 399
Qy 415 IleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSer-----GlnSerLeu 431
Db 400 TATACTCGAGGTCTCTTGCACTCCAACTTTTGGTTCTTCCGAATTTTCGAAGCTCTT 459
Qy 432 AsnLeuValPhe-----AspGluAlaSerSerGlyAsnValVal 444
Db 460 ACTCAAGCTTACAAAGATCATGCTCAACAGCATAGTCTGTCTCAATGACAGCTTCCT 519
Qy 445 SerGlyLys-----AspAlaAlaPheSerValTyrGlnArgProLeuAsnArgLys 461
Db 520 AATTCTCGACCGATCGACGAAATCACCTTTTCTACAATCGACAGGCGG----- 567
Qy 462 AspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeuLeu 481
Db 568 AAATCTCTTAGTCAGCTAACTTCCATCTGCTTGGTGAGACTTGGATTGAATATTCAA----- 621

QY	482	AsnLysLysAlaAlaGlnLeuAsnThrGlnAspGlyLysSer---GluGlnPheArgSer	500
DB	622	---GAGGCTCATGCTTCTCTACCGCGATGCTTCTCTCTCGATGATTT---	669
QY	501	CysValAlaSerProTyrSerValGlnSerThrProPheValGluAsnValProLeu	520
DB	670	---GTTGTTGATGGCTGGTGGCAGGAGGATCAACCTTGTTCMAACAG---	714
QY	521	SerHisIleSerHisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisPro	540
DB	715	AAATCTATCACTTCTTTCGAGCATGACAAATCAACCAACGAGCTG---	759
QY	541	ArgValAspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysPro	560
DB	760	---CTACCT---GCTGTGTTGAAATACCT	783
QY	561	AsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTyrThrAspLeuAspLeuArg	580
DB	784	ACGGAT-----GGAAGTATGATGGGAAATGACATGAAGCAGCTCAAAATTGAA	834
QY	581	GluLysIleGlyAlaGlySerPheGlyThrValTyrArgGlyGlyTrpHisGlySerAsp	600
DB	835	AAAAGGTGGCATGTGGATCATACGGGGAACTATTAGAGGAACCTATTGTAGTCAGAA	894
QY	601	ValAlaValLysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeu	620
DB	895	GTAGCTATCAAAATCTCAAGCCTGAGCGTGTAAATCGGAAATGCTACGAGATTTCT	954
QY	621	ArgGluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAla	640
DB	955	CAGAAAGTATATATAATAGAGAAAGTTGGCAATAAAATGTGTCCAGTTCAITGTGCA	1014
QY	641	ValThrLysProProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyr	660
DB	1015	TGTACAGCATCAACCAACCTCTGCATTGTGCACAGAGTTCATGACTCGGGAGCATTTAT	1074
QY	661	ArgLeuLeuHisLys-----SerGlyValLysAspIleAspGluThrArgArgIleAsnMet	679
DB	1075	GATTTCTCTCAACCAACCAAGGGGTTTTAAATTCATCTTTG-----CTCAAGTG	1128
QY	680	AlaPheAspValAlaLysGlyMetAsnTyrLeuHisArgArgAspProIleValHis	699
DB	1129	GCATCTGAGCTCTCGAAGGAATGAATATTCATCAAAACAAT-----ATTATTCAT	1182
QY	700	ArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThrValLysValCysAsp	719
DB	1183	ACAGACCTTAAGACTGCTTAATCTCTTATGGACCAACATGAAGTGTGCAAGTTGCCGAT	1242
QY	720	PheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaIleGlyThr	739
DB	1243	TTTGTGTTCGACAGTTCAGACTGAGTCAGGGGTATTGACA---GCGGAAACAGGGACA	1299
QY	740	ProGluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspVal	759
DB	1300	TACCATGGATGGCTCCAGAGGTCATTGAGCACAACCTTATGATCAGCGGAGATGTC	1359
QY	760	TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTyrCysAsnLeu	779
DB	1360	TTACAGTACCGATGTGCTGTGGAACTTTTGACTGGGGAATCCCATATTCTTACTTG	1419
QY	780	AsnProAlaGlnValValAlaValGlyPheLysGlyArgLeuAspIleProArg	799
DB	1420	ACTCCACTCCAAAGCTGCTGTGGCGTTGTCCAAAAGGACATTAGACCAAAATTTCCAAG	1479
QY	800	AspValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLys	819
DB	1480	GAACACACCCAAACTGACTGAACTTCTTGAGAAATCTGCGACGACAGCCAGCTCTA	1539
QY	820	ArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGln	836
DB	1540	AGACCAATTTTGCAGAAATCATAGAAATGCTTAACCAACTAATCCCGAG	1590

RESULT 7

US-09-938-842A-903

Sequence 903, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPT300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 903

LENGTH: 1638

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-903

Alignment Scores:

Score:	Pred. No.:	Length:
Percent Similarity:	1.06e-44	1638
Best Local Similarity:	513.00	Matches: 157
Query Match:	43.74%	Conservative: 84
DB:	28.45%	Mismatches: 149
	11.57%	Indels: 163
	10	Gaps: 18

US-09-904-389-2 (1-850) x US-09-938-842A-903 (1-1638)

QY	345	ProCysArgIleAlaLysGlyCysLys-----	353
DB	201	CCCTGCCAGTAGTCTTTGGATGTGAATGTGGAGAGCGCTGAAGAGCGTCTTGATGCACAA	260
QY	354	-----TyrCysThrArgAspAlaSerSerCysLeuValArgPhe-----	367
DB	261	GCAGATTGCTGCATTCTGCTTAGCATGCCAGATCCGCGCTGCTATCG-AGATTTCATCTCG	319
QY	368	-----	368
DB	320	TCCAGCGTGCATCTTCATCTTTATGTTTGCCTCTTTTGTCAACTTTTGATTCCTCGG	379
QY	369	LeuAspArgGluTyrLeuLeuAspLeuIleGlyArg-----ProGlyCysLeuCys	385
DB	380	CTCACAGGTTCTTTCGTCTACTCCTCTTTCTTAAGGTTCAACCTGCCGGATCTCTGCTG	439
QY	386	GlnProAspSerLeuLeuAsn-----GlyProSerSerIleSerIleSer	400
DB	440	ACTTG-GACTCTACTTCTAATCATGCTGGTCATTTCTCTCTACCCGAAAAAGCATTCAT	498
QY	401	SerProLeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeu	420
DB	499	CCGCGCGCTCCCTTTGGTTTCATCCCGCTTAATCTTTGAAGCAGCTTGCACTTCGACGTAGTTTA	558
QY	421	AlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSerSer	440
DB	559	TCCCAA-----	579
QY	441	GlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArgProLeuAsnArg	460
DB	580	AACCTCTGTTTCATACCAAT-----TCACCTCTATTCCAGCGCCCTTGCAAT---	621
QY	461	LysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeu	480
DB	622	-----GAGATACCTTTCCACAGAAGCAACGCTAAACTCCCTTTTCAG	666

QY 724 gLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrProGluTrpMetAl 744
Db 426 GTTCCATAACCATACA-----ACACACATGCTCTGTTGGAACTTTCCCATGGATGGC 373
QY 744 aProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPheGlyVa 764
Db 372 TCCAGAAGTATATCCAGAGTCTCCCTGTCAGAACTTTGTGACACATATTCCTATGTTGT 313
QY 764 lileLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnVa 784
Db 312 GGTCTCTGGAGAGTCTCAACAAGGAGGTCCTCCCTTTAAAGGTTTGGAAAGATTACCAAGT 253
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 252 AGCTTGGCTTGTAGTGGAAAAAAGACGAGAGATTACCATTCGAAGCAGTTCGCCCAAG 193
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArgProSerPheSe 824
Db 192 TTTTGTGACTGTTACATCAGTGTGGAGAGCTGTGCGAAGCTGATGCCAAGAACGCCATATTCAA 133
QY 824 rSerIleMetGluThrLeuLysProMetThr 834
Db 132 GCAATCATTTCAATCTCGAGTCCATGTCA 102

RESULT 9
US-09-757-982-6
; Sequence 6, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2001-01-10
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1365)
US-09-757-982-6

Alignment Scores:
Pred. No.: 6.53e-44 Length: 1365
Score: 504.50 Matches: 112
Percent Similarity: 55.84% Conservative: 41
Best Local Similarity: 40.88% Mismatches: 106
Query Match: 11.38% Indels: 15
DB: 9 Gaps: 4

US-09-904-389-2 (1-850) x US-09-757-982-6 (1-1365)
QY 564 SerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluIysIle 583
Db 7 TCTCTCGTGCTCTCTTGTGCAAAATTAATTTGATGACTTGCAGTCTTTTGAAGAACTGC 66
QY 584 GlyAlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAsp-----Val 601
Db 67 GGTGGAGAACTTTTGGAGTGTATTCAGCCCAATGGATATCAAGACACAGAGGTTG 126
QY 602 AlaValIysIleLeuTrpGluAsnAspPheHisProGluArgValAsnGluPheLeuArg 621
Db 127 GCTGTAAGAGCTCTCCAAATAGAG-----AAA 156
QY 622 GluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaVal 641
Db 157 GAGGCAAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTCTTATGAGTAAT 216

QY 642 ThrLysProProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArg 661
Db 217 CTTGAACCTCCCAACTATGCGATGTGCACAGAAATATGCTTCTCTGGATCATTCTATGAT 276
QY 662 LeuLeuHisLysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPhe 681
Db 277 TACATTAAACAGTAAACAGAGTGGAGAGATGATGATGATGATGATGATGATGATGATGAT 336
QY 682 AspValAlaLysGlyMetAsnTyrLeuHisArgAspPro---ProIleValHisArg 700
Db 337 GATGTAGCCAAAGAAATGCAATTATTACATATGAGAGCTCCTCTCAAGGTGATTCACAGA 396
QY 701 AspLeuLysSerProAsnLeuValAspLysLysTyrThrValLysValCysAspPhe 720
Db 397 GACCTCAAGTCAAGAACGTTGTTATAGTCTGATGAGTACTGAGATCTGTGACTTT 456
QY 721 GlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrPro 740
Db 457 GGTGCTCTCGTTCCTAACCATACA-----ACACACATGCTCTTGGTGGAACTTTC 510
QY 741 GluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyr 760
Db 511 CCATGATGCTCCAGAGTTATCCAGAGTCTCCTGTGCAGAACTTGTGCACACATAT 570
QY 761 SerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsn 780
Db 571 TCCTATGCTGTGTTCTCTGGAGATGCTAACAAGGAGGTCCTCTTTAAAGGTTTGGAA 630
QY 781 ProAlaGlnValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAsp 800
Db 631 GGATTACAGTAGCTGCTGTGTAGTGGAAAAAAGACGAGAGATTACCAATTCAGAGCAGT 690
QY 801 ValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArg 820
Db 691 TGCCCCAGAAAGTTTGTCTGAACTGTATCATCAGTGTGGGAAAGCTGATGCCAAGAAACGG 750
QY 821 ProSerPheSerSerIleMetGluThrLeuLysProMetThr 834
Db 751 CCATCATTCACCAAAATCATTTCAATCTCGAGTCCATGTCA 792

RESULT 10
US-09-757-982-4
; Sequence 4, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2001-01-10
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(1411)
US-09-757-982-4

Alignment Scores:
Pred. No.: 1.3e-43 Length: 2120
Score: 504.50 Matches: 112
Percent Similarity: 55.84% Conservative: 41
Best Local Similarity: 40.88% Mismatches: 106
Query Match: 11.38% Indels: 15
DB: 9 Gaps: 4

US-09-904-389-2 (1-850) x US-09-757-982-4 (1-2120)

QY 564 SerLeuGlyLeuGluAspLeuValIleProThrAspLeuAspLeuArgGluLysIle 583
Db 53 TCCTCGGCGCTCTTGTGCAAAATTAATTTGATGACTGTCAGTTTGTGAAACTGC 112
QY 584 GlyAlaGlySerPheGlyThrValTyrArgGlyGluThrPheHisGlySerAsp-----Val 601
Db 113 GGTGGAGGAAGTTTGGGAGTGTATTGAGCAAAATGGATATCACAGGCAAGAGGAGTG 172
QY 602 AlavalIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArg 621
Db 173 GCTGTAAAGAGCTCTCAAAATAGAG-----AAA 202
QY 622 GluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyValaVal 641
Db 203 GAGCGCAAAATATCAGTCTCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAAT 262
QY 642 ThrLysProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArg 661
Db 263 CTGGAACCTCCCACTATGCGCATTTGCAGANATGCTTCTGGGATCACTCTATGAT 322
QY 662 LeuLeuHisLysSerGlyValLysAspLeuAspGluThrArgArgIleAsnMetAlaPhe 681
Db 323 TACATTAAACAGTAACAGAGAGTGCAGAGATGGATGATGATATGATACCTGGCCACT 382
QY 682 AspValAlaLysGlyMetAsnTyrLeuHisArgAspPro---ProIleValHisArg 700
Db 383 GATGAGCCAAAGGATGCATTATTACATATGAGGCTCTCTGCAAGGTGATTCACAGA 442
QY 701 AspLeuLysSerProAsnLeuValAspLysLysTyrThrValLysValCysAspPhe 720
Db 443 GACCTCAAGTCAAGAAACCTTTTATAGCTCTGATGAGTACCTGAGATCTGTGACTTT 502
QY 721 GlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrPro 740
Db 503 GGTGCTCTCGGTTCCATAACCATACA-----ACACACATGCTCTGTGGTGGACTTTC 556
QY 741 GluTyrMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyr 760
Db 557 CCATGATGCTCCAGAGTATTCAGAGTCTCCCTGTGTCAGAACTTGTGACACATAT 616
QY 761 SerPheGlyValIleLeuTyrGluLeuAlaThrLeuGlnGlnProTyrCysAsnLeuAsn 780
Db 617 TCCTATGGTGTGTTCTCTGGAGATGCTAACAGGGAGGTCCTTTAAAGGTTTGGAA 676
QY 781 ProAlaGlnValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAsp 800
Db 677 GGATTAAGTAGCTGTGGCTTGTAGTGAAAGAAACAGAGATTAACCATTCACAGCAGT 736
QY 801 ValAsnProLysLeuAlaSerLeuIleValAlaCysTyrPalaAspGluProTyrLysArg 820
Db 737 TGCCCCAGAAAGTTTGTGCACTGTTACATCAGTGTGGGAGCTGATGCCAAGAACGG 796
QY 821 ProSerPheSerSerIleMetGluThrLeuLysProMetThr 834
Db 797 CCATCATTAAGCAAAATCAATTCATCTGGAGTCCATGTCA 838

RESULT 11

US-09-917-800A-1405
; Sequence 1405, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1405
; LENGTH: 2719
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 M15428
US-09-917-800A-1405
Alignment Scores:
Pred. No.: 2,5e-40 Length: 2719
Score: 475.50 Matches: 130
Percent Similarity: 53.26% Conservative: 74
Best Local Similarity: 33.94% Mismatches: 134
Query Match: 10.72% Indels: 45
DB: 10 Gaps: 13
US-09-904-389-2 (1-850) x US-09-917-800A-1405 (1-2719)
QY 474 LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly 493
Db 842 AGAGAAAGGAAATGAATTTCTGGAACCTTAAGTGTACTCTTGAAGAAACAAAGAGAGAG 901
QY 494 LysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSerThrProPhe 513
Db 902 GATGCAATTCGAAGTCACAGTGAATCAGCCTCACTTCAGCCCTGTCCAGCAGCCCC--- 958
QY 514 ValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHis 533
Db 959 ---AACAACTCGAGCCCA----- 973
QY 534 LeuLeuAlaLeuSerHisProArgMetAspHisValaAsnAsnLeuProPheValHisGly 553
Db 974 ---ACAGGCTGTGTACAGCCCAAAACCCCTGTGCCAGCACAAAGAGAGAGGGCCAGGA 1030
QY 554 SerGlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuValIlePro 573
Db 1031 TCTGGGACCCAGGAAACAAATATTAGGCTCTGTGGGCGAGAGAGATTCAAGTTATTATC 1090
QY 574 Trp-----ThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGly 589
Db 1091 TGGAAATAGAACCCAGTCAGGTGATGCTGTACTCGATTGTCTCGGCTCCTTTGGC 1150
QY 590 ThrValTyrArgGlyGluThrPheHisGlySerAspAlaValLysIleLeuThrGluGln 609
Db 1151 ACTGTGTACAGGGCAAGTGGCATGGA---GATGTGTGAGTAAAGATCTCTAAAGGTGGTT 1207
QY 610 AspPheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeu 629
Db 1208 GACCCAACTCCAGAGCAACTTCAGGCCCTTCAGAAACAGAGGTGGCTGTGTTGGCCAAACA 1267
QY 630 ArgHisProAsnIleValLeuPheMetGlyValaValThrLysProProAsnLeuSerIle 649
Db 1268 CGCATGTTAATCTGCTGTTCATGGGGTACATGACAAG---GACAACCTGGCGATT 1324
QY 650 ValThrGluTyrIleuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLys 669

```
Db 1325 GTACCCAGTGGTGTGAAGCAGCAGTCTCTACAAACACCTGCTCAT----- 1369
Qy 670 AspileAspGluThrArg-----ArgIleAsnMetAlaPheAspValAla 684
Db 1370 ---GTCAGAGAGACCAAAATCCAGATGTTCCAGCTAAATTGACATTTGCCCGCAGACAGCT 1426
Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProProlleValHisArgAspLeuLysSer 704
Db 1427 CAGGGAATGACATATTACATGCAAGAAGAC-----ATCATCCAGAGACATGAATCC 1480
Qy 705 ProAsnLeuValAspLysTyrThrValLysValCysAspPheGlyLeuSerArg 724
Db 1481 AACAAATATTTTCCATGAAGCCCTCACGGTGAATAATCGGAGATTTGGTTGGCAACA 1540
Qy 725 LeuLysAlaAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742
Db 1541 GTGAAGTCGGCTGGAGTGGTTCTCAGCAGGTGTAACAGCCCACTGGCTGTGTGTGG 1600
Qy 743 MetAlaProGluValLeuArg-----AspGluProSerAsnGluLysSerAspVal 759
Db 1601 ATGGCCCCAGAGTAATCCGAATGCGAGGATACACCCGTTGAGCTTCAGTTCAGTCCGATGTC 1660
Qy 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779
Db 1661 TACTCTATGTCATGTTGCTGTATGAGCTGATGACTGGGGGCTTCCCTACTCCACATC 1720
Qy 780 AsnProAla---GlnValValAlaAlaValGlyPheLysGlyLysArgLeuAspIlePro 798
Db 1721 AACACCCGAGACCATCATCTTCATGTTGGGGCGGTGAGTCCCTCCCATCATCTTAGC 1780
Qy 799 ArgAspValAsn-----ProLysLeuAlaSerLeuIleValAla---CysTrpAlaAsp 815
Db 1781 AGGCTCTACAGAACTGCCCCAGGCAATGAGAGGTTGGTGGCTGACTGTGTGAAGAAA 1840
Qy 816 GluProTrpLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLys 835
Db 1841 GTCAAAGAAGAAGGCGCTTTGTTTCTCAGATCTCTGCTTCCATGAGCTGCTTCAGCAC 1900
Qy 836 GlnAlaPro 838
Db 1901 TCTCTGCGG 1909

RESULT 12
US-10-440-341-6
; Sequence 6, Application US/10440341
; Publication No. US20030181413A1
; GENERAL INFORMATION:
; APPLICANT: RAPP, ULF
; APP, HARALD
; STORM, STEPHEN M.
; TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/440,341
; FILING DATE: 15-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/748,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
```

```
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683/82731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-440-341-6

Alignment Scores:
Pred. No.: 8,07e-40 Length: 2229
Score: 469.50 Matches: 143
Percent Similarity: 51.24% Conservative: 84
Best Local Similarity: 32.28% Mismatches: 168
Query Match: 10.53% Indels: 51
DB: 12 Gaps: 16

US-09-904-389-2 (1-850) x US-10-440-341-6 (1-2229)
Qy 419 SerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAla 438
Db 693 TCTTTAGCAGAGATGCCCTAACATCTGATCTGCATCCCTTCGGCACCCGCTCGGACTCT 752
Qy 439 SerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal---TyrGlnArgPro 457
Db 753 ATTTGGGCCCCAAATTTCTCACCAGTCCTCTCTCTCAAAATCCATTCCTCAATTTCCACAGCCC 812
Qy 458 LeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsn 477
Db 813 TTCCGACACGAGATGAAGATCATCGAAT-----CAATTGGGCAACGAGACCGATCC 866
Qy 478 SerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly----- 493
Db 867 TCATCAGTCCCAAT-----GTGCATATAAACAACAATAGAACCTGTCAATATTGAT 917
Qy 494 -----LysSerGluGlnPheArgSerCysValAlaAlaSerProTyrSerValGlnSer 510
Db 918 GACTTGATTAGACACAGGATTTCTGGTGTATGGAGGATCAACACAGGTTTGTCTGCT 977
Qy 511 ThrPro-----PheValGluAsnValValProLeuSerHisIleSer 524
Db 978 ACCCCCTCGCTCAATTACCTACCTACCTAACTAACTGAA-AGCCTTACAGAAATCTCC 1036
Qy 525 HisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisProArgMetAspHis 544
Db 1037 AGGACCTC-AGCGAAGAAAGAAAGTCACTCT-----CATCTCAGAGACAGAGA 1083
Qy 545 ValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysProAsnGluLeuSer 564
Db 1084 ATCGAATGAAACACACTTGGTAGACGGAGCTCGAGT----- 1118
Qy 565 LeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIleGly 584
Db 1119 -----GATGATTGGGAGATTCTGATGGCGAGATTACAGTGGGACAAAGAAATTGGA 1169
Qy 585 AlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLys 604
Db 1170 TCTGGATCATTTGGACAGCTACAGAGGAAGTGGCATGGT---GATGTGCGACGTGAAA 1226
Qy 605 IleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAla 624
Db 1227 ATGTTGAATGTGACAGCACCTACACCTCAGCAGCTTCAAGAGCCTTCAAAATGAAGTAGGA 1286
Qy 625 IleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyValAlaValThrLysPro 644
```

```

Db 1287 GTACTCAGGAAAACACGACATGTGAATATCTCTACTCTTTCATGGGTATTCCCAAG--- 1343
Qy 645 ProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHis 664
Db 1344 CCACAATGGCTATTGTATCCAGTGGTGTGAGGGCTCCAGCTTGTATCACCATCTCCAT 1403
Qy 665 LysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAla 684
Db 1404 ATCATTTGAGACCAA---TTTGAGATGATCAATCAATTTATAGATTATTCACGACAGACTGCA 1460
Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProProIleValHisArgAspLeuLysSer 704
Db 1461 CAGGCGATGATTAATCTACAGCCCAAGTCA-----ATCATCCACAGAGACCTCAAGAGT 1514
Qy 705 ProAsnLeuLeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArg 724
Db 1515 AATAATATTTCTTCATGAGACCTCACAGATAAATAAGTGAATTTTGGTCTAGCTACA 1574
Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTyr 742
Db 1575 GTGAATCTGATGGAGTGGTCCCATCAGTTTGAACAGTTGTCTGATCCATTTTGTGG 1634
Qy 743 MetAlaProGluValLeuArgAspGluProSerAsnGlu-----LysSerAspVal 759
Db 1635 ATGGCACCAGGAATCATCAGAAATGCAAGATAAATAATCCATACAGCTTTTCAGTCAGATGA 1694
Qy 760 TyrSerPheGlyValIleLeuTyrGluLeuAlaThrLeuGlnGlnProTyrCysAsnLeu 779
Db 1695 TATGATTTGGAATGTTCTGTATGATTAATGATGACTGGACAGTACCTTATTCACACATC 1754
Qy 780 AsnProAla---GlnValAlaAlaVal-----GlyPheLysGlyLysArgLeuAsp 796
Db 1755 AACACACAGGACCAAGATAATTTTATGTTGGGACGAGGATACCTGTCTCCAGATCTCAGT 1814
Qy 797 IleProArgAspValAsnProLys---LeuAlaSerLeuIleValAlaCysTrpAlaAsp 815
Db 1815 AAGGTACGAGTAATCTCCAAAGCCATGAAGAGATTAATGGCAGAGTCCCTCAAAAG 1874
Qy 816 GluProTyrLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLys 835
Db 1875 AAAAGAGATGAGAGACCACTCTTCCCAAAATTTCTCGCTCTATTGAGCTGCTGGCCCGC 1934
Qy 836 GlnAlaPro 838
Db 1935 TCATTGCCA 1943

RESULT 13
US-10-057-550-89
; Sequence 89, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 89
; LENGTH: 2510
```

```

; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
US-10-057-550-89

Alignment Scores:
Pred. No.: 9,73e-40 Length: 2510
Score: 469.50 Matches: 143
Percent Similarity: 51.24% Conservative: 84
Best Local Similarity: 32.28% Mismatches: 168
Query Match: 10.59% Indels: 51
DB: 14 Gaps: 16

US-09-904-389-2 (1-850) x US-10-057-550-89 (1-2510)
Qy 419 SerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAla 438
Db 974 TCCTTAGCAGAGACTCCCTAACATCTGATCATCTCCCTCCGACCCGCTCGGACTCT 1033
Qy 439 SerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal---TyrGlnArgPro 457
Db 1034 ATTGGGCCCCAATTCTCACCAGTCGCTCTCCTTCAAAATCCATTCCAATTCCACAGCCC 1093
Qy 458 LeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsn 477
Db 1094 TTCGACCCAGCAGATGAAGATCATCGAAT-----CAATTGGGCAACGAGACCGATCC 1147
Qy 478 SerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly----- 493
Db 1148 TCATCAGCTCCCAAT-----GTGCATATAAACAATAAGAACCTGTCAATATTGAT 1198
Qy 494 -----LysSerGluGlnPheArgSerCysAlaLaserProTyrSerValGlnSer 510
Db 1199 GACTTGATTAGACCAAGGATTTCTGTGTGATGGAGATCAACACAGGTTGTCTGCT 1258
Qy 511 ThrPro-----PheValGluAsnValValProLeuSerHisIleSer 524
Db 1259 ACCCCCTCCCTCATTACCTGCTCACTAACTAAGTGAAG-AGCCTTACAGAAATCTCC 1317
Qy 525 HisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisProArgMetAspHis 544
Db 1318 AGGACCTC-AGCGAGAAAGGAAGTATCTTT-----CCTCTCAGAAAGACAGA 1364
Qy 545 ValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysProAsnGluLeuSer 564
Db 1365 ATCGAATGAAAACACTTGGTAGACGGGACTCGAGT----- 1399
Qy 565 LeuGlyLeuGluAspLeuValIleProTyrThrAspLeuAspLeuArgGluLysIleGly 584
Db 1400 -----GATGATTGGGAGATTCTCTGATGGCAGATTACAGTGGGCAAGAATTGGA 1450
Qy 585 AlaGlySerPheGlyThrValTyrArgGlyGluTyrHisGlySerAspValAlaValLys 604
Db 1451 TCTGGATCATTTGGACAGACTCACAGGGAAGTGGCATGCT---GATGTGGCAGTGAAG 1507
Qy 605 IleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAla 624
Db 1508 ATGTTGAATGTGCACAGCACCTTACACCTCAGCAGATTCAACCTTCAAAATGAAGTAGGA 1567
Qy 625 IleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysPro 644
Db 1568 GTACTCAGAAAACACGACATGTGAATATCTCTCTTCATGGGCTATTCCACAAAG--- 1624
Qy 645 ProAsnLeuSerIleValThrGlyLysSerArgGlySerLeuTyrArgLeuLeuHis 664
Db 1625 CCACAACCTGGCTATTGTTACCCAGTGGTGAAGGCTCCAGGCTGTATACCTATCTCCAT 1684
Qy 665 LysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAla 684
Db 1685 ATCATTTGACACCAA---TTTGAGATGATCAACTATAGATATTGACACAGACTGCA 1741
Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProIleValHisArgAspLeuLysSer 704
```

Db 1742 CAGGGCATGATTAAGTACACCCCAAGTCA-----ATCATCCACAGAGACCTCAAGAGT 1795
Qy 705 ProAsnLeuValAspLysLysThrValLysValCysAspPheGlyLeuSerArg 724
Db 1796 AATAATATATTTCTTCATGACGACCTCACAGTAAATAATAGGTGATTTGGTCTAGCTACA 1855
Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742
Db 1856 GTGAATCTCGATGGAGTGGGTCCTCATCAGTTTGAACAGTGTGTCTGGATCCATTTTGTGG 1915
Qy 743 MetAlaProGluValLeuArgAspGluProSerAsnGlu-----LysSerAspVal 759
Db 1916 ATGGCACACAGAGTCAATCAGATGCAAGATAAATCCATACAGCTTTTCAGTCAAGATGTA 1975
Qy 760 TyrSerPheGlyValLeuThrGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779
Db 1976 TATGCAATTTGGGATTTGCTGTATGAATTCAGTACTGGACAGTTTACCTTTATTTCAAACATC 2035
Qy 780 AsnProAla---GlnValValAlaAlaVal-----GlyPheLysGlyLysArgLeuAsp 796
Db 2036 AACACAGGGACAGATATTTTATGTGGGACGAGGATACCTGTCTCCAGATCTCAGT 2095
Qy 797 IleProArgAspValAsnProLys---LeuAlaSerLeuLeuValAlaCysTrpAlaAsp 815
Db 2096 AAGGTACGGAGTAACCTCTCAAAAGCCATCAAGAGATTAATGGCAGAGTGGCTCAAAAAG 2155
Qy 816 GluProTrpLysArgProSerPheSerIleMetGluThrLeuLysProMetThrLys 835
Db 2156 AAAAGATGAGAGACCACTCTTTCCCAANTTTCGGCTCTATTGAGCTGTGGCCCGC 2215
Qy 836 GlnAlaPro 838
Db 2216 TCATTGCCA 2224

RESULT 14

US-10-173-225B-67
; Sequence 67, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0665
; CURRENT APPLICATION NUMBER: US/10/173,225B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 67
; LENGTH: 2510
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-173-225B-67

Alignment Scores:
Pred. No.: 9.73e-40 Length: 2510
Score: 469.50 Matches: 143
Percent Similarity: 51.24% Conservative: 84
Best Local Similarity: 32.28% Mismatches: 168
Query Match: 10.59% Indels: 51
Gaps: 14

US-09-904-389-2 (1-850) x US-10-173-225B-67 (1-2510)
Qy 419 SerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAla 438
Db 974 TCCTTAGCAGAGACTGCCCTAAACATCTGGATCATCCCTTCCGACCCCGCTCGGACTCT 1033
Qy 439 SerSerGlyAsnValSerGlyLysAspAlaAlaPheSerVal---TyrGlnArgPro 457
Db 1034 ATGGGGCCCCAAATCTCACCGCTCCCTTCAAAATCCATTCCAATTCACAGCCC 1093
Qy 458 LeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyLysLysAspArgAsn 477
Db 1094 TTCCGACGACGAGATGAAGATCATCGAAAT-----CAATTTGGGCAACGAGACCGATCC 1147
Qy 478 SerGlnLeuLeuAsnLysLysAlaGlnLeuAsnThrGlnAspGly----- 493
Db 1148 TCATCAGCTCCCAAT-----GTGCATATAACACATAGAACCTGTCAATATTGAT 1198
Qy 494 -----LysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
Db 1199 GACTTTGATTAGACCAAGGATTTCTGGTGTGATGGAGGATCAACACACAGGTTTGTCTGCT 1258
Qy 511 ThrPro-----PheValGluAsnValValProLeuSerHisIleSer 524
Db 1259 ACCCCCTGCTCTATACCTGGCTCTACTACTAACGTGAA-AGCCTTACAGAAATCTCC 1317
Qy 525 HisIleGlySerGluAspSerGluHisLeuAlaLeuSerHisProArgMetAspHis 544
Db 1318 AGGACCTC-AGCGAGAAAGGAGTCATCTT-----CATCTCAGAAAGACAGGA 1364
Qy 545 ValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysProAsnGluLeuSer 564
Db 1365 ATCGAATGAACACATCTGTAGACGGGACTCGAAT----- 1399
Qy 565 LeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIleGly 584
Db 1400 -----GATGATTGGAGATTCCTGATGGGAGATTTACAGTGGGACACAAAGATTTGA 1450
Qy 585 AlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLys 604
Db 1451 TCTGGATCATTTTGGACAGCTCTACAGGAAAGTGGCATGCT---GATGTGGCAGTGA 1507
Qy 605 IleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAla 624
Db 1508 ATGTTGAATGTGACAGCCTACACTCAGCAGTTACAAGCCTTCAAAATGAAGTAGGA 1567
Qy 625 IleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysPro 644
Db 1568 GTACTCAGGAAACACGACATGTGAATATCTCTCTTCATGGGCTATTCCACAAAG--- 1624
Qy 645 ProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHis 664
Db 1625 CCNACTGGCTATTGTTACCCAGTGGTGTGAGGGCTCCAGCTTGTATCCACTCTCCAT 1684
Qy 665 LysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAla 684
Db 1685 ATCATTGACACCAAAA---TTTGAGATGATCAAACTTATAGATATTGACGACAGCTGCA 1741
Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProProIleValHisArgAspLeuLysSer 704
Db 1742 CAGGGCATGATTTACTTACACCCCAAGTCA-----ATCATCCACAGAGACTCAAGAGT 1795
Qy 705 ProAsnLeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArg 724
Db 1796 AATAATATATTTCTTCATGAAGACCTCACAGTAAATAATAGGTGATTTTGGTCTAGCTACA 1855
Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742
Db 1856 GTGAATCTCGATGGAGTGGGTCCTCATCAGTTTGAACAGTGTGTCTGGATCCATTTTGTGG 1915
Qy 743 MetAlaProGluValLeuArgAspGluProSerAsnGlu-----LysSerAspVal 759
Db 1916 ATGGCACAGAGTCAATCAGATGCAAGATAAATCCATACAGCTTTTCAGTCAAGATGTA 1975

Search completed: October 24, 2003, 05:09:58
Job time : 1001 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2742.5	61.8	821	1	US-07-928-464-2	Sequence 2, Appli
2	2742.5	61.8	821	1	US-08-003-311B-2	Sequence 2, Appli
3	2742.5	61.8	821	1	US-08-261-432-2	Sequence 2, Appli
4	2742.5	61.8	821	5	PCI-US93-07347-2	Sequence 5, Appli
5	191.5	26.9	263	3	US-09-035-706-5	Sequence 5, Appli
6	1191.5	26.9	263	3	US-08-955-841-5	Sequence 5, Appli
7	1191.5	26.9	263	3	US-09-390-425-5	Sequence 5, Appli
8	1191.5	26.9	263	4	US-09-566-908-5	Sequence 5, Appli
9	504.5	11.4	455	3	US-09-221-233-5	Sequence 5, Appli
10	504.5	11.4	455	3	US-09-221-928-5	Sequence 5, Appli
11	504.5	11.4	455	3	US-09-221-527-5	Sequence 5, Appli
12	504.5	11.4	455	3	US-09-221-236-5	Sequence 5, Appli
13	504.5	11.4	455	3	US-09-221-416-5	Sequence 5, Appli
14	504.5	11.4	455	3	US-09-221-245-5	Sequence 5, Appli
15	504.5	11.4	455	3	US-09-163-115-5	Sequence 5, Appli
16	504.5	11.4	455	3	US-09-221-528-5	Sequence 5, Appli
17	504.5	11.4	455	3	US-09-593-553-5	Sequence 5, Appli
18	504.5	11.4	455	3	US-09-221-237-5	Sequence 5, Appli
19	504.5	11.4	455	4	US-09-399-588-2	Sequence 2, Appli
20	483	10.9	1584	4	US-09-457-040B-27	Sequence 27, Appli
21	468	10.6	648	1	US-08-185-282-4	Sequence 4, Appli
22	467.5	10.5	765	4	US-09-886-319A-8	Sequence 8, Appli
23	465	10.5	648	1	US-08-185-282-1	Sequence 1, Appli
24	464	10.4	648	1	US-08-185-282-2	Sequence 2, Appli
25	460	10.4	648	1	US-08-185-282-3	Sequence 3, Appli
26	460	10.4	659	4	US-09-886-319A-7	Sequence 7, Appli
27	457.5	10.3	648	1	US-08-376-151-2	Sequence 2, Appli

Db 545 DIPWCDLNKEIKGAGSFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLR 604
 Qy 631 HNVILFMGAVTKPPNLSIVTYLRSGLYRLLLHKSQVKD-IDETRINNAFVAKGMNY 699
 Db 605 HNVILFMGAVTQPPNLSIVTYLRSGLYRLLLHKSQVAREQDERRRLSMAYDVAKGMNY 664
 Qy 690 LHRDPPIVHRDLKSPNLLVDKXYTVKVCDFGLSRLKARTFLSKSAAGTPEWMAPEVLR 749
 Db 665 LHRNPPPIVHRDLKSPNLLVDKXYTVKVCDFGLSRLKASTFLSKSAAGTPEWMAPEVLR 724
 Qy 750 DEPSNEKSDVYSGVILWELATLQOPWCMNLAQVVAAGVKGKRLDIPRDNVPLASLI 809
 Db 725 DEPSNEKSDVYSGVILWELATLQOPWCMNLAQVVAAGVKGKRLDIPRDNVPLASLI 784
 Qy 810 VACWADEPWKRPFSFSSIMETLKPMTKQAPPQOSRTD 845
 Db 785 EGCWTNEPWKRPFSFATIMDLLRLPLIKSAVPPPNRSD 820

RESULT 3

US-08-261-432-2
 ; Sequence 2, Application US/08261432
 ; Patent No. 5603322
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, Joseph R.
 ; APPLICANT: Kieber, Joseph J.
 ; TITLE OF INVENTION: Constitutive Triple Response Gene
 ; TITLE OF INVENTION: and Mutations
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
 ; ADDRESSEE: No. 560322ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/261,432
 ; FILING DATE: June 17, 1994
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/003,311
 ; FILING DATE: January 12, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lori Y. Beardsell
 ; REGISTRATION NUMBER: 34,293
 ; REFERENCE/DOCKET NUMBER: JPN-1864
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 821 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-261-432-2

Query Match 61.8%; Score 2742.5; DB 1; Length 821;
 Best Local Similarity 62.3%; Pred. No. 3.2e-237;
 Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;
 Qy 1 MEMPGRRSDYSLLSQIPDEEVG-----TGASTSFYDSVAA-----GGNVIKRTDR-VFD 49
 Db 1 MEMPGRRSNYLLSQFSDQVSVSVTGAPPPHYDLSSENNSNHNHSGNTGKAKAERGDF 60

Qy 50 WD-----GSGDRLNTQAYRIQ-NLY-SWIGLQHSAGSSVDDSSLSDDYIYAPTLSHPAAN 103
 Db 61 WDPSSGGGGDRLANQPNRVGNMNYASSLGLQSGSGSFGESLSDGYTMYPTLS-AAAN 119
 Qy 104 BINALEYLLDDDFV-----MKAVGGG-SSGKSWAQOQTEESFOLQOPLVRL 150
 Db 120 EIBSVFPQDQDFLFGGGGGDURIQMAADSGAGSSGKSWAQOQTEESYQLQALALRL 179
 Qy 151 SDDXTCADDPNFMDPIFDEAALRSLSABEASHRFVWNGCMYLEKVPDGFYLIHGMOP 210
 Db 180 SSEATCADDPNFDPVDESALRTSPSSAETVSHRFVWNGCLSYDKVPDGFYMMGLDP 239
 Qy 211 YWISLCTNLQEDGRIPESLKTVDSSIGSIEVVLDRHSDASLKLQNRVHNISSCV 270
 Db 240 YWTLCIDLHESGRIPESLRAVDGSDGSLEAIIVDRSRDPFKELEHNRVHDISCCI 299
 Qy 271 TTKEVADHIAKLVNHLGSSVSEGEDVLVSAWKECSDDLKECLGSAVIPLCSLSVGLCRH 330
 Db 300 TTKEVVDQLAKLICNRMGGPVIMGEDELVPMWKECIDGLKE-IFKVVPVIGSLSVGLCRH 358
 Qy 331 RALLFKVLADSIDLPCRIACKGKYCTRDDASSCLVRFGLDREYLDLIGRPGCLCOPDSL 390
 Db 359 RALLFKVLADIIDLPCRIACKGKYCNRDDAASCLVRFGLDREYLDLVGPKHLEWEPDSL 418
 Qy 391 LNPSSISISSPLRPPRLKPIESTIDFSLAKQYFLDSQSLNLFVDEASSGNVYSGDAA 450
 Db 419 LNPSSISISSPLRPPRPKPEPAVDPELLAKQYFSDSQSLNLFVDFASD-----DMG 471
 Qy 451 FSVYORPLNRKVDGKTIWVGDKDRNSQLLNKAAQLNTODGKSEQFRSCVASPYVQS 510
 Db 472 FSVFROYDNPQENDALAENG-----GS 496
 Qy 511 TPFVENVPLSHISHIGSEDSHLLALSHPRMDHVNLPFVHGSQILRKPNELSLGLEDL 570
 Db 497 LPSSANWP-----QNMWASNOIEAAPMNAPI-SQVPVNRANRELGLDGDMM 544
 Qy 571 VIPWTDLUREKIGAGSGFTVVRGWHGSDVAVKILTEODFHPERVNEFLREVAIMKSLR 630
 Db 545 DIPWCDLNKEIKGAGSFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLR 604
 Qy 631 HNVILFMGAVTKPPNLSIVTYLRSGLYRLLLHKSQVKD-IDETRINNAFVAKGMNY 689
 Db 605 HNVILFMGAVTQPPNLSIVTYLRSGLYRLLLHKSQVAREQDERRRLSMAYDVAKGMNY 664
 Qy 690 LHRDPPIVHRDLKSPNLLVDKXYTVKVCDFGLSRLKARTFLSKSAAGTPEWMAPEVLR 749
 Db 665 LHRNPPPIVHRDLKSPNLLVDKXYTVKVCDFGLSRLKASTFLSKSAAGTPEWMAPEVLR 724
 Qy 750 DEPSNEKSDVYSGVILWELATLQOPWCMNLAQVVAAGVKGKRLDIPRDNVPLASLI 809
 Db 725 DEPSNEKSDVYSGVILWELATLQOPWCMNLAQVVAAGVKGKRLDIPRDNVPLASLI 784
 Qy 810 VACWADEPWKRPFSFSSIMETLKPMTKQAPPQOSRTD 845
 Db 785 EGCWTNEPWKRPFSFATIMDLLRLPLIKSAVPPPNRSD 820

RESULT 4

PCT-US93-07347-2
 ; Sequence 2, Application PC/TUS9307347
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, Joseph R.
 ; APPLICANT: Kieber, Joseph J.
 ; TITLE OF INVENTION: Constitutive Triple Response Gene and
 ; TITLE OF INVENTION: Mutations
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
 ; ADDRESSEE: Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.

```

1 ZIP: 19103
2
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: PatentIn Release #1.0, Version #1.25
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: PCT/US93/07347
10 FILING DATE: 19930805
11 CLASSIFICATION:
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Miller, Suzanne E.
14 REGISTRATION NUMBER: 32,279
15 REFERENCE/DOCKET NUMBER: UPN-1086
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 215-568-3100
18 INFORMATION FOR SEQ ID NO: 2:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 821 amino acids
21 TYPE: amino acid
22 TOPOLOGY: linear
23 MOLECULE TYPE: protein
24 PCT-US93-07347-2

```

Query Match	61.8%;	Score	2742.5;	DB 5;	Length	821;			
Best Local Similarity	62.3%;	Pred. No.	3.2e-237;						
Matches	546;	Conservative	99;	Mismatches	144;	Indels	87;	Gaps	14;
QY	1	MEMGRSDYSLLSQIPDEEVG-----TGASTSFYDSVAA-----GGNVIKGRTDR-VFD	49						
DBb	1	MEMGRSNTYLLSQFSDQVSVSVTCAPPHYDLSLSSSENRSNHNSGNTGKAKASRGCFD	60						
QY	50	WD---GSGDRLNTOAVRIG-NLY-SWIGLQRHSSGVSDDSSLSDDSYAATLSPNPAAN	103						
DBb	61	WDPSCGGGGDRLNQNPRVGNVNYASSLGLQRQSSGSGFGESSLSCGYMPTLS-AAAN	119						
QY	104	EINALEYILDDFRV-----MKAVGSGG--SSGKSWAQQTSEESFQIQPLVIRL	150						
DBb	120	EIESVGFQDDGFLRGLFGGGGDLRIQMAADSAAGSSSGKSWAQQTSEESYQQLALAIRL	179						
QY	151	SSDTCADDPNFMDPIPEAALRSLISAIAISHRFWNGCMSEYIEKVPDGFYLIHGMDP	210						
DBb	180	SSEATCADDPNFLOVPDESALRTPSSAETVSHRFWNGCLSYDKVPDGFYMGNGLDP	239						
QY	211	YVWSLCTNLOQDGRIPFESLTKTVDSIGSSIEVWLIDRHSASLIKELQNRVHNLSSCV	270						
DBb	240	YIWTUCIDLRHSGRIPSTIESLRAVDGVSLSRAIVDRRSSDPAPFKELHNRVHDISCSCI	299						
QY	271	TKTEVADHIAKLVNCHLGGVSEGEDVLVAWEKCSDDLKECLGSAVIPCLSLSVGLCRH	330						
DBb	300	TKTEVVDQALAKLINCRMGGPVMGEDLVPMWKECIDGLKE-IFKVVVPIGLSVGLCRH	358						
QY	331	RALLFKVLADSIDLPCRIAGCKYCTRDDASSCLVRFGLDREYILDLIGRPCLCQPSL	390						
DBb	359	RALLFKVLADIIDLPCRIAGCKYCNRDDAASCLVRFGLDREYILDLVKGPHLEPDSL	418						
QY	391	LNGPSSISISPLAPPRLKPIESTIDPSRLAKOYFIDDSGLNLVPTDEASGNVWSGKAA	450						
DBb	419	LNGPSSISISPLFPFPKPEPAVDPELLAKOYFSDOSLNLVDFPARD-----DMG	471						
QY	451	FSVYQRPVLRNRKDVQKGTIVVTGDKRNSQLLNKAAQLANTQDKSQRFSCVSPYSVQS	510						
DBb	472	FSMFHRQYDNPGGENDALAENG-----GS	496						
QY	511	TPFENVVPLSHISHIGSEDSHELLALSHPRMDHVNNLPFHGSQLIRKPNELSLGLEDL	570						
DBb	497	LPSANMPP-----QNMRASNQIEAAPMNAFPISQFVPNRANRELJGDGDDM	544						
QY	571	VIPWTDLRLREKIGAGSGFTYRGWEHGSVDVAKILTEQDFHPFRVNETFLREVALMKSLR	630						
DBb	545	DIPWCDLNIKEKIGAGSGFTVHRAEWEGSDVAVKILMEQDFHAERVNETFLREVALMKSLR	604						
QY	631	HPNIVLFGAVTKPPNLSIVTEYLSRGSRLYRLLHKSQVKD-IDETERINNDPVAKGMY	689						

691	HRDPP	IVHRDLKSPNLLVDK	YTVKVCDFGLSRLKARTFLSKSAAGTPEWMAPEVL	RD	750
	:	:	:	:	
121	HRNPPIVHRDLKSPNLLVDK	YTVKVCDFGLSRLKASTFLSKSAAGTPEWMAPEVL	RD	180	
	:	:	:	:	
751	EPSNEKSDVYFSGVILWELATL	QOPWGNLNPQAVAAVGFCKGRIDLPRDYNPKL	ASTIV	810	
	:	:	:	:	
181	EPSNEKSDVYFSGVILWELATL	QOPWGNLNPQAVAAVGFCKGRLEIPNLNPFQVA	ALIE	240	
	:	:	:	:	
811	ACWADEPWKPSPFSSIMETL	KPM	833		
	:	:	:	:	
241	GCWTNEPWKPSPFATIMDL	LRPL	263		
	:	:	:	:	
db	:	:	:	:	

RESULT 6
 US-08-955-841-5
 ; Sequence 5, Application US/08955841
 ; Patent No. 6013782
 ; GENERAL INFORMATION:
 ; APPLICANT: Dedhar, Shoukat
 ; APPLICANT: Hannigan, Greg
 ; TITLE OF INVENTION: Integrin-Linked Kinase and
 ; TITLE OF INVENTION: its Uses
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bozicevic & Reed, LLP
 ; STREET: 285 Hamilton Avenue, Suite 200
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Fastseq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/955,841
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sherwood, Pamela J
 ; REGISTRATION NUMBER: 36,677
 ; REFERENCE/DOCKET NUMBER: KIN-2CIP1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-327-3400
 ; TELEFAX: 650 327-3231
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 263 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-955-841-5

	Query Match	26.9%;	Score 1191.5;	DB 3;	Length 263;
	Best Local Similarity	84.4%;	Pred. No. 9.7e-99;		
	Matches 222;	Conservative 25;	Mismatches 15;	Indels 1;	Gaps 1;
Qy	572	I PWTDLDRXIGAGSGCTVYRGPHGSDYAVKILTEQDFPHERVNEFLREVAINMKSIRH	631		
		: :			
Dd	1	I PWCPLNTEKXIGAGSGFTVHRAEWHGSDYAVKILMEQDFFHAERVNEFLREVAINMKRLRH	60		
		: :			
Qy	632	PNVLFMGAVTKPNNLSIVTLEYLRSGLSYLLHLKHSGVKD-IDETRINMAFDVAKGMMYL	690		
		: :			
Dd	61	PNVLFMGAVTQPNNLSIVTLEYLRSGLSYLLHLKHSGARQLDERRLSWAYDVAKGMMYL	120		
		: :			
Qy	691	HRRDPPIVHRDLKSNPLLVDKKYTKVCDFGLSRLKARTFLSKSAAGTPPEWMAPEVLR	750		

```

121 HNANPPVHRDLKSPNLLVDKKYTVVKVOCDFGLSRUKASTFLSSKSAGTPWMAPEVLRD 180
      | : |||||
751 EPSNEKSDVYSFQVILWEIATLQQPWCMLNPAQVVAAVGFGKGRLDIPRDNYPKLASLIIV 810
      | |||||
181 EPSNEKSDVYSFQVILWEIATLQQPWGNLNPAQVVAAVGFGKGLEIPRNLPNPQAAIE 240
      | |||||
811 ACWADBPWKGPDPSPSSIMETIKPM 933
      | :|||
241 GCWTNBPWKGPSPATMDLLRLPL 263
      | :|||

```

```

RESULT 7
US-09-390-425-5
; Sequence 5, Application US/09390425
; Patent No. 6338958
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/390,425
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: US60/009,074
; EARLIER FILING DATE: 1995-12-21
; EARLIER APPLICATION NUMBER: US08/752,345
; EARLIER FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 263
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(263)
US-09-390-425-5

```

Query Match	26.3%	Score 1191.5	DB 4	Length 263
Best Local Similarity	84.4%	Pred. No. 9.7e-99		
Matches 222	Conservative 25	Mismatches 15	Indels 1	Gaps 1
QY	572	IPWTDLDLRKIGAGSGFTGYRGEWHGSDVAVKILTEQDFHPERVNEFLREVAIMKSLRH	631	
		1 IPWCDLNKEKIGAGSGFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKSLRH	60	
Db				
QY	632	PNIVLFWGATVKPPNISIVTEYLSRGSILYRLAHKSGVD-IDETFRINMAEDVAKGNNYL	690	
Db	61	PNIVLFWGATVQPPNISIVTEYLSRGSILYRLAHKSGAREQDERRRLSMAIDVAKGNNYL	120	
QY	691	HRRDPFVHRLDLKSPNLLVDKYYTKVCFGLSRLKARTFLLSSKSAAGTTPSWMAPEVLR	750	
Db	121	HNRNPPVHRLDLKSPNLLVDKYYTKVCFGLSRLKASTFLLSSKSAAGTTPSWMAPEVLR	180	
QY	751	EPSNEKSDVTSFGVILWELATLOOPNCNLPAAQVAAVGFKGKRLIDIRDVNPKLASIV	810	
Db	181	EPSNEKSDVTSFGVILWELATLOOPMGNLNPAAQVAAVGFCKRLLEIPNLNFPVAAILE	240	
QY	811	ACWADEPWKSPFSSIMETLKPM	833	
Db	241	GCWTNEPWKSPFATIMDLLRPL	263	

```

RESULT 8
US-09-566-906-5
; Sequence 5, Application US/09566906
; Patent No. 6369205
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/566.906

```



```
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-527-5

Query Match      11.4%; Score 504.5; DB 3; Length 455;
Best Local Similarity 40.9%; Pred. No. 1.2e-36;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SIGLEDLVIPWTDLDLREKIGAGSGFTVYRGWHGSD--VAVKILTEQDFHPRVNEFLR 621
DB 3 SLGASFVQIKFDDLOFFENC GGSGFSGVYRAKWSIQDKQEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSYLRLHKSQVGDIDETRINMAF 681
DB 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLSDYINSRSEEMDMHMTWAT 112

QY 682 DVAKGMNVLHRRDP-PIVHRDLKSNLVDKKTYYKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKVIHRDLKSNRVVIAADGVLIKICDFGASRFNHT--THMSLVGTF 170

QY 741 ENMAPEVLDRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVAAVGFKGKLDIPRD 800
DB 171 PNMAPEVIQSLPVSETCDTYSYGVVLEWMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSPSSIMETLKPMT 834
DB 231 CPRSFAELLHQCEWADAKKRPSPKQIISLESMS 264

RESULT 12
US-09-221-236-5
; Sequence 5, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-236-5

Query Match      11.4%; Score 504.5; DB 3; Length 455;
Best Local Similarity 40.9%; Pred. No. 1.2e-36;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SIGLEDLVIPWTDLDLREKIGAGSGFTVYRGWHGSD--VAVKILTEQDFHPRVNEFLR 621
DB 3 SLGASFVQIKFDDLOFFENC GGSGFSGVYRAKWSIQDKQEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSYLRLHKSQVGDIDETRINMAF 681
DB 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLSDYINSRSEEMDMHMTWAT 112

QY 682 DVAKGMNVLHRRDP-PIVHRDLKSNLVDKKTYYKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKVIHRDLKSNRVVIAADGVLIKICDFGASRFNHT--THMSLVGTF 170

QY 741 ENMAPEVLDRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVAAVGFKGKLDIPRD 800
DB 171 PNMAPEVIQSLPVSETCDTYSYGVVLEWMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSPSSIMETLKPMT 834
DB 231 CPRSFAELLHQCEWADAKKRPSPKQIISLESMS 264

RESULT 13
US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-416-5

Query Match      11.4%; Score 504.5; DB 3; Length 455;
Best Local Similarity 40.9%; Pred. No. 1.2e-36;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SIGLEDLVIPWTDLDLREKIGAGSGFTVYRGWHGSD--VAVKILTEQDFHPRVNEFLR 621
DB 3 SLGASFVQIKFDDLOFFENC GGSGFSGVYRAKWSIQDKQEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSYLRLHKSQVGDIDETRINMAF 681
DB 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLSDYINSRSEEMDMHMTWAT 112

QY 682 DVAKGMNVLHRRDP-PIVHRDLKSNLVDKKTYYKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKVIHRDLKSNRVVIAADGVLIKICDFGASRFNHT--THMSLVGTF 170

QY 741 ENMAPEVLDRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVAAVGFKGKLDIPRD 800
DB 171 PNMAPEVIQSLPVSETCDTYSYGVVLEWMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSPSSIMETLKPMT 834
DB 231 CPRSFAELLHQCEWADAKKRPSPKQIISLESMS 264

RESULT 14
US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-245-5

Query Match      11.4%; Score 504.5; DB 3; Length 455;
Best Local Similarity 40.9%; Pred. No. 1.2e-36;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SIGLEDLVIPWTDLDLREKIGAGSGFTVYRGWHGSD--VAVKILTEQDFHPRVNEFLR 621
DB 3 SLGASFVQIKFDDLOFFENC GGSGFSGVYRAKWSIQDKQEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSYLRLHKSQVGDIDETRINMAF 681
DB 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLSDYINSRSEEMDMHMTWAT 112

QY 682 DVAKGMNVLHRRDP-PIVHRDLKSNLVDKKTYYKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKVIHRDLKSNRVVIAADGVLIKICDFGASRFNHT--THMSLVGTF 170

QY 741 ENMAPEVLDRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVAAVGFKGKLDIPRD 800
DB 171 PNMAPEVIQSLPVSETCDTYSYGVVLEWMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSPSSIMETLKPMT 834
DB 231 CPRSFAELLHQCEWADAKKRPSPKQIISLESMS 264
```


Db 3 SLGASPVQIKFDDLOFFENC GGSGSVYRAKWI SQDKSEVAVKLLKIE-----K 52
Qy 622 EVAIMKSLRHPNTVLPFGAVTKPPNLSIVTEYLSRGSLYRLHLKSGVKDIDETRRINMAP 681
Db 53 EABILSVLSHRNIIQFYGVILEPPNYGIVTEYASIGSLYDYINSNRSEEMDMOHIMTWAT 112
Qy 682 DVAKGMNLYLHRRDP-PIVHRDLKSNLLVDKKTWKVCD FGLSR LKARTFLSSKSAAGTP 740
Db 113 DVAKGMNLYLHRRDP-PIVHRDLKSNLLVDKKTWKVCD FGLSR LKARTFLSSKSAAGTP 740
Qy 741 EWMAPVLRDEPNKSDVYSGVILWELATLQOPWCNLPNPAQVVAAGVPGKGLDIPRD 800
Db 171 PMAPEVIQSLPVSETCDTYSYGVVLWMLTREVFPFKGLEGLQVAVLWVEKNERLTIPSS 230
Qy 801 VNPKLASLIVACWADEPKRPSFSSIMETLKPM 834
Db 231 CPRSFAELLHQWEADAKKRPSPFKQIISLESMS 264

RESULT 15

US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NKL-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-115-5

Query Match 11.4%; Score 504.5; DB 3; Length 455;
Best Local Similarity 40.9%; Pred. No. 1.2e-36;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
Qy 564 SLGLEDLVIPWTDLDLREKIGAGSGTGYVYRGSGHSD--VAVKILTBODFHPERVNEFLR 621
Db 3 SLGASPVQIKFDDLOFFENC GGSGSVYRAKWI SQDKSEVAVKLLKIE-----K 52
Qy 622 EVAIMKSLRHPNTVLPFGAVTKPPNLSIVTEYLSRGSLYRLHLKSGVKDIDETRRINMAP 681
Db 53 EABILSVLSHRNIIQFYGVILEPPNYGIVTEYASIGSLYDYINSNRSEEMDMOHIMTWAT 112
Qy 682 DVAKGMNLYLHRRDP-PIVHRDLKSNLLVDKKTWKVCD FGLSR LKARTFLSSKSAAGTP 740
Db 113 DVAKGMNLYLHRRDP-PIVHRDLKSNLLVDKKTWKVCD FGLSR LKARTFLSSKSAAGTP 740
Qy 741 EWMAPVLRDEPNKSDVYSGVILWELATLQOPWCNLPNPAQVVAAGVPGKGLDIPRD 800
Db 171 PMAPEVIQSLPVSETCDTYSYGVVLWMLTREVFPFKGLEGLQVAVLWVEKNERLTIPSS 230
Qy 801 VNPKLASLIVACWADEPKRPSFSSIMETLKPM 834
Db 231 CPRSFAELLHQWEADAKKRPSPFKQIISLESMS 264

Search completed: October 23, 2003, 17:26:12
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2003, 17:25:12 ; Search time 38 Seconds
(without alignments)
3745.830 Million cell updates/sec

Title: US-09-904-389-2

Perfect score: 4435

Sequence: 1 MEMPGRRSDYSLLSQIPDEE.....KPMTKQAPPOQSRITDLSVM 850

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4433	100.0	850	10	US-09-904-389-2
2	2742.5	61.8	821	12	US-10-171-404A-48
3	1191.5	26.9	263	10	US-09-840-704-5
4	504.5	11.4	349	15	US-10-106-698-6345
5	504.5	11.4	455	9	US-09-757-982-5
6	467.5	10.5	650	12	US-10-440-341-7
7	467.5	10.5	765	12	US-10-376-564-8
8	460	10.4	659	12	US-10-376-564-7
9	457.5	10.3	425	9	US-09-828-313-29
10	457.5	10.3	648	10	US-09-513-145-6
11	457.5	10.3	648	12	US-10-440-341-3
12	457.5	10.3	648	15	US-10-059-585-38
13	456	10.3	271	10	US-09-840-704-6
14	455	10.3	256	12	US-09-976-782-40
15	455	10.3	257	12	US-09-976-782-29

16	453	10.2	1130	12	US-10-171-889-1	Sequence 1, Appli
17	453	10.2	1130	12	US-10-263-480-2	Sequence 2, Appli
18	452	10.2	1130	12	US-10-204-041-4	Sequence 4, Appli
19	448	10.1	394	10	US-09-862-027-19	Sequence 19, Appl
20	444.5	10.0	746	15	US-10-153-668-436	Sequence 436, App
21	444.5	10.0	859	15	US-10-153-668-324	Sequence 324, App
22	444.5	10.0	892	15	US-10-153-668-438	Sequence 438, App
23	444	10.0	1567	12	US-10-312-318-2	Sequence 2, Appli
24	444	10.0	1594	12	US-10-312-318-4	Sequence 4, Appli
25	440	9.9	847	14	US-10-143-133-2	Sequence 2, Appli
26	438	9.9	1036	12	US-10-354-358-24	Sequence 24, Appl
27	438	9.9	1036	14	US-10-014-882-2	Sequence 2, Appli
28	437.5	9.9	257	11	US-09-823-187-46	Sequence 46, Appl
29	436	9.8	252	12	US-09-976-782-41	Sequence 41, Appl
30	436	9.8	254	12	US-09-976-782-30	Sequence 30, Appl
31	433.5	9.8	651	14	US-10-186-399-2	Sequence 2, Appli
32	433	9.8	966	10	US-09-771-161A-197	Sequence 197, App
33	432	9.7	675	9	US-09-977-269-4	Sequence 4, Appli
34	432	9.7	675	10	US-09-977-260-4	Sequence 4, Appli
35	432	9.7	675	11	US-09-977-261-4	Sequence 4, Appli
36	432	9.7	675	12	US-10-021-560-108	Sequence 108, App
37	432	9.7	675	14	US-10-186-399-3	Sequence 3, Appli
38	432	9.7	686	15	US-10-220-501-12	Sequence 12, Appl
39	424	9.6	604	15	US-10-205-342-1	Sequence 1, Appli
40	420	9.5	606	12	US-10-440-341-5	Sequence 5, Appli
41	417	9.4	251	8	US-08-987-689A-32	Sequence 32, Appl
42	417	9.4	251	15	US-10-292-524-32	Sequence 32, Appl
43	413	9.3	537	12	US-09-976-782-85	Sequence 85, Appl
44	408.5	9.2	1036	10	US-09-771-161A-255	Sequence 255, App
45	408.5	9.2	1036	10	US-09-771-161A-256	Sequence 256, App

ALIGNMENTS

RESULT 1

```
US-09-904-389-2
; Sequence 2, Application US/09904389
; Patent No. US2002012940A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Schuster, Debra K.
; TITLE OF INVENTION: CTBL HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (154)...(154)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-904-389-2
```

Query Match	100.0%;	Score 4433;	DB 10;	Length 850;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 850;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEMPGRRSDYSLLSQIPDEE	VGTGASTSFYD	SVAGGNVTKGTRDVFWDGSGDHLNT 60
DB	1	MEMPGRRSDYSLLSQIPDEE	VGTGASTSFYD	SVAGGNVTKGTRDVFWDGSGDHLNT 60
QY	61	QAYRIGNLYMIGLQRRHSSGSSYDD	SSLSDDYAPTLSNPAANEINALEY	ILDDDDFRVMK 120
DB	61	QAYRIGNLYMIGLQRRHSSGSSYDD	SSLSDDYAPTLSNPAANEINALEY	ILDDDDFRVMK 120
QY	121	AVGGSGSGKSWAQCTTESFQ	LQPLVRLSSDXTCCADDNFMDP	DPDEALRSLISAE 180

Db 121 AVSGSGSSKWAQTEESFQLOQLVLRLSSDXTCADPMPPIPEAALRLSISAE 180
Qy 181 AISHRFVWNGMSYLBKVPDGYLHGMDDPYVWSICTNLQEDGRIPSPESLKTVDSSIGS 240
Db 181 AISHRFVWNGMSYLBKVPDGYLHGMDDPYVWSICTNLQEDGRIPSPESLKTVDSSIGS 240
Qy 241 SIEVLIIDRHSASLAKELQNRVHNTSSSCVTTKEVADHIAKLVNHLGSGVSEGEDDLS 300
Db 241 SIEVLIIDRHSASLAKELQNRVHNTSSSCVTTKEVADHIAKLVNHLGSGVSEGEDDLS 300
Qy 301 AWKECSDDLKELGSAVIFLCSLSVGLCHRRALLFKVLADSIDPCRIACKCYCTRDDA 360
Db 301 AWKECSDDLKELGSAVIFLCSLSVGLCHRRALLFKVLADSIDPCRIACKCYCTRDDA 360
Qy 361 SSCVLFGLDREYLDLGRPGCLQDPSLLNGPSSISISSPLRPKPIESTIDFRSL 420
Db 361 SSCVLFGLDREYLDLGRPGCLQDPSLLNGPSSISISSPLRPKPIESTIDFRSL 420
Qy 421 AKQYFLDSQSLNLFVDEASGNVVGKDAAFVYQRPVPLNRKDVQKTIIVTGDKNRNSQL 480
Db 421 AKQYFLDSQSLNLFVDEASGNVVGKDAAFVYQRPVPLNRKDVQKTIIVTGDKNRNSQL 480
Qy 481 LNKKAQQLNTODGSKSOFSCVSPVSVQSTPFFVENVPLSHISHIGSEDSEHLLALSH 540
Db 481 LNKKAQQLNTODGSKSOFSCVSPVSVQSTPFFVENVPLSHISHIGSEDSEHLLALSH 540
Qy 541 RMDVNNLPVHSGSLIRKPNLSLGLDLVLPWTDLDLREKIGAGSGTGYRGEMGSD 600
Db 541 RMDVNNLPVHSGSLIRKPNLSLGLDLVLPWTDLDLREKIGAGSGTGYRGEMGSD 600
Qy 601 VAKKILTEQDFHPRVNEFLREVAIMKSLRHNPVLFMGAVTKPNNLSIVTEYLSRGLY 660
Db 601 VAKKILTEQDFHPRVNEFLREVAIMKSLRHNPVLFMGAVTKPNNLSIVTEYLSRGLY 660
Qy 661 RLLHKSQKDIIDTRINMAFVAKGMNVLHRRDPPVHRRDLKSNLLVDKKTIVKVCDF 720
Db 661 RLLHKSQKDIIDTRINMAFVAKGMNVLHRRDPPVHRRDLKSNLLVDKKTIVKVCDF 720
Qy 721 GLRLKARTFLSKSAAGTPEWMAPEVLRDPSNEKSDVYSGVILWELATLQOPWNCNLN 780
Db 721 GLRLKARTFLSKSAAGTPEWMAPEVLRDPSNEKSDVYSGVILWELATLQOPWNCNLN 780
Qy 781 PAQVVAAGFKGRLDIPRDVNPFLASLIVACWADEPKRPSFSSIMETLKPMTKQAPPQ 840
Db 781 PAQVVAAGFKGRLDIPRDVNPFLASLIVACWADEPKRPSFSSIMETLKPMTKQAPPQ 840
Qy 841 QSRDTLSVM 850
Db 841 QSRDTLSVM 850

RESULT 2

US-10-171-404A-48
; Sequence 48, Application US/10171404A
; Publication No. US20030177529A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
; FILE REFERENCE: 16313-0119
; CURRENT APPLICATION NUMBER: US/10/171,404A
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: 60/295,680
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-171-404A-48
Query Match 61.8%; Score 2742.5; DB 12; Length 821;

Best Local Similarity 62.3%; Pred. No. 1.6e-219;
Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;
Qy 1 MEMPCRDRDYSLLSQIPDEEVG---TCASTSPYDVSAA-----GGNVTKGRTDR-VFD 49
Db 1 MEMPCRDRDYSLLSQIPDEEVG---TCASTSPYDVSAA-----GGNVTKGRTDR-VFD 49
Qy 50 WD---GSGDHRHTQAVRIQ-NLY-SWIGLQRHSGSSYDDSSLSDDYYAPTLNPAAN 103
Db 61 WDPSSGGGGDHRHTQAVRIQ-NLY-SWIGLQRHSGSSYDDSSLSDDYYAPTLNPAAN 103
Qy 104 EINALLEYLDDDFV-----MKAVSGG-SSGKSWAQOOTESFOLQOPLVLRL 150
Db 120 EIESYGFQDDGFLRGFGGGGDLRIQMAADASGSSGSKSWAQOOTESFOLQOPLVLRL 179
Qy 151 SDDXTCADPMPPIPEAALRLSISAEAIASHRFVWNGMSYLBKVPDGYLHGMDDP 210
Db 180 SDEATCADPMPPIPEAALRLSISAEAIASHRFVWNGMSYLBKVPDGYLHGMDDP 239
Qy 211 YWVSLCTNLQEDGRIPSPESLKTVDSSIGSIEVLIIDRHSASLAKELQNRVHNTSSCV 270
Db 240 YIWTLCIDLHESGRIPSPESLKTVDSSIGSIEVLIIDRHSASLAKELQNRVHNTSSCV 299
Qy 271 TTKEVADHIAKLVNHLGSGVSEGEDDLVSAWKBCSDDLKELGSAVIFLCSLSVGLCRH 330
Db 300 TTKEVADHIAKLVNHLGSGVSEGEDDLVSAWKBCSDDLKELGSAVIFLCSLSVGLCRH 358
Qy 331 RALLFKVLADSIDPCRIACKCYCTRDDASSCLVRFGLDREYLDLIGRPGCLQDPSL 390
Db 359 RALLFKVLADSIDPCRIACKCYCTRDDASSCLVRFGLDREYLDLIGRPGCLQDPSL 418
Qy 391 LNPSSISISGPLPPLPKPIESTIDFRSLAKQVFLDSQSLNLFVDEASGNVVGKDA 450
Db 419 LNPSSISISGPLPPLPKPIESTIDFRSLAKQVFLDSQSLNLFVDEASGNVVGKDA 471
Qy 451 FSVYQRPVNRKDVQKTIIVTGDKNRNSQLNKKAQQLNTODGSKSOFSCVSPVSVQ 510
Db 472 FSVYQRPVNRKDVQKTIIVTGDKNRNSQLNKKAQQLNTODGSKSOFSCVSPVSVQ 510
Qy 511 TPFVNVVPLSHISHIGSEDSEHLLALSHPRMDHVNLPFVHSGSLIRKPNLSLGLDL 570
Db 497 LPPSANMPP-----QNMWRASNQTEAAPMKNAPISQPVVPEANRELGLDGD 544
Qy 571 VTPWTDLDLREKIGAGSGTGYRGEMGSDVAVKILTEQDFHPRVNEFLREVAIMKSLR 630
Db 545 DIPWCDLNIKEKIGAGSGTGYRGEMGSDVAVKILTEQDFHPRVNEFLREVAIMKSLR 604
Qy 631 HPNIVLFMGAVTKPNNLSIVTEYLSRGLYRLHKSAGREQLDERRRLSKWYDVAKGM 689
Db 605 HPNIVLFMGAVTKPNNLSIVTEYLSRGLYRLHKSAGREQLDERRRLSKWYDVAKGM 664
Qy 690 LHRDPPIVHRDLKSNLLVDKKTIVKVCDFGLSRLKARTFLSKSAAGTPEWMAPEVLR 749
Db 665 LHRDPPIVHRDLKSNLLVDKKTIVKVCDFGLSRLKARTFLSKSAAGTPEWMAPEVLR 724
Qy 750 DEPSNEKSDVYSGVILWELATLQOPWNCNLNPAQVVAAGFKGRLDIPRDVNPFLASLI 809
Db 725 DEPSNEKSDVYSGVILWELATLQOPWNCNLNPAQVVAAGFKGRLDIPRDVNPFLASLI 784
Qy 810 VACWADEPKRPSFSSIMETLKPMTKQAPPQSRD 845
Db 785 EGCWITNEPKRPSFSSIMETLKPMTKQAPPQSRD 820
RESULT 3
US-09-840-704-5
; Sequence 5, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Incegrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON

* CURRENT APPLICATION NUMBER: US/09/840,704
* CURRENT FILING DATE: 2001-04-23
* PRIOR APPLICATION NUMBER: 09/566,906
* PRIOR FILING DATE: 2000-05-09
* PRIOR APPLICATION NUMBER: US08/752,345
* PRIOR FILING DATE: 1996-11-19
* NUMBER OF SEQ ID NOS: 16
* SOFTWARE: FastSeq for Windows Version 4.0
* SEQ ID NO 5
* LENGTH: 263
* TYPE: PRT
* ORGANISM: H. sapiens
* FEATURE:
* NAME/KEY: Other
* LOCATION: (1)...(263)
US-09-840-704-5

Query Match 26.9%; Score 1191.5; DB 10; Length 263;
Best Local Similarity 84.4%; Pred. No. 5.6e-91;
Matches 222; Conservative 25; Mismatches 15; Indels 1; Gaps 1;

QY 572 IPWTDLRLREKIGAGSGFTYRGWEGSDVAVKILTEQDFHPRVNEFLREVAINKSLRH 631
DB 1 IPWCDLNKEKIGAGSGFTYRGWEGSDVAVKILMEQDFHAERYNEFLREVAINKSLRH 60
QY 632 PNIVLFMGAVTKPNLSIVTEYLSRGLYRLHLKSGVKD-IDETRRINMAFDVAKGMNYL 690
DB 61 PNIVLFMGAVTQPNLSIVTEYLSRGLYRLHLKSGAREQLDERRLSNAYDVAKGMNYL 120
QY 691 HRDPPVHRDLKSNLLVDKKTIVKVCDFGLSRKARTFLSKSAAGTPPEMAPEVLRL 750
DB 121 HNRNPPVHRDLKSNLLVDKKTIVKVCDFGLSRKASTFLSKSAAGTPPEMAPEVLRL 180
QY 751 EPSNEKSDVYSFGVILWELATLQOPWNCNLPAAQVAAVGFKGKRLDIDPRDVNPKLASLIV 810
DB 181 EPSNEKSDVYSFGVILWELATLQOPWNCNLPAAQVAAVGFKGKRLDIDPRDVNPKLASLIV 240
QY 811 ACWADEPKRPFSSIMETLKP 833
DB 241 GCWTNEPKRPFSSIMETLKP 263

RESULT 4
US-10-106-698-6345
* Sequence 6345, Application US/10106698
* Publication No. US20030109690A1
* GENERAL INFORMATION:
* APPLICANT: Ruben et al.
* TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
* FILE REFERENCE: PA003P1
* CURRENT APPLICATION NUMBER: US/10/106,698
* CURRENT FILING DATE: 2002-03-27
* PRIOR APPLICATION NUMBER: PCT/US00/26524
* PRIOR FILING DATE: 2000-09-28
* PRIOR APPLICATION NUMBER: US 60/157,137
* PRIOR FILING DATE: 1999-09-29
* PRIOR APPLICATION NUMBER: US 60/163,280
* PRIOR FILING DATE: 1999-11-03
* NUMBER OF SEQ ID NOS: 8564
* SOFTWARE: Patent In Ver. 3.0
* SEQ ID NO 6345
* LENGTH: 349
* TYPE: PRT
* ORGANISM: Homo sapiens
* FEATURE:
* NAME/KEY: MISC FEATURE
* LOCATION: (340)
* OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6345

Query Match 11.4%; Score 504.5; DB 15; Length 349;
Best Local Similarity 40.9%; Pred. No. 1.6e-33;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVIPWTDLRLREKIGAGSGFTYRGWEGSD--VAVKILTEQDFHPRVNEFLR 621
DB 59 SLGASVQIKFDDLOFFENCNGGSGFVSYRAKWISQDKKEVAVKLLKIE-----K 108
QY 622 EVAIMKSLRHPNIVLFMGAVTKPNLSIVTEYLSRGLYRLHLKSGVKDIDETRRINMAF 681
DB 109 EABILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGLSYDYINSNRSEEMDMHMTWAT 168
QY 682 DVAKGMNYLHRRDP-PIVHRDLKSNLLVDKKTIVKVCDFGLSRKARTFLSKSAAGTP 740
DB 169 DVAKGMNYLHRRDP-PIVHRDLKSNLLVDKKTIVKVCDFGLSRKARTFLSKSAAGTP 226
QY 741 ENMAPEVLDEPSNEKSDVYSFGVILWELATLQOPWNCNLPAAQVAAVGFKGKRLDIDPRD 800
DB 227 PWAPEVIQSLFVSETCDTYSYGVVLEWMLTREVFPFKGLEGLQVAVLWVVEKNERLTIPSS 286
QY 801 VNPKLASLIVACWADEPKRPFSSIMETLKPMT 834
DB 287 CPRSFAELLHQCEADAKKRPSPFKQIISILESMS 320

RESULT 5
US-09-757-982-5
* Sequence 5, Application US/09757982
* Patent No. US20020094559A1
* GENERAL INFORMATION:
* APPLICANT: Acton, Susan
* TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
* FILE REFERENCE: MNI-050
* CURRENT APPLICATION NUMBER: US/09/757,982
* CURRENT FILING DATE: 2001-01-10
* PRIOR APPLICATION NUMBER: 09/163,115
* PRIOR FILING DATE: 1998-09-29
* NUMBER OF SEQ ID NOS: 15
* SOFTWARE: Patent In Ver. 2.0
* SEQ ID NO 5
* LENGTH: 455
* TYPE: PRT
* ORGANISM: Homo sapiens
US-09-757-982-5

Query Match 11.4%; Score 504.5; DB 9; Length 455;
Best Local Similarity 40.9%; Pred. No. 2.4e-33;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVIPWTDLRLREKIGAGSGFTYRGWEGSD--VAVKILTEQDFHPRVNEFLR 621
DB 3 SLGASVQIKFDDLOFFENCNGGSGFVSYRAKWISQDKKEVAVKLLKIE-----K 52
QY 622 EVAIMKSLRHPNIVLFMGAVTKPNLSIVTEYLSRGLYRLHLKSGVKDIDETRRINMAF 681
DB 53 EABILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGLSYDYINSNRSEEMDMHMTWAT 112
QY 682 DVAKGMNYLHRRDP-PIVHRDLKSNLLVDKKTIVKVCDFGLSRKARTFLSKSAAGTP 740
DB 113 DVAKGMNYLHRRDP-PIVHRDLKSNLLVDKKTIVKVCDFGLSRKARTFLSKSAAGTP 170
QY 741 ENMAPEVLDEPSNEKSDVYSFGVILWELATLQOPWNCNLPAAQVAAVGFKGKRLDIDPRD 800
DB 171 PWAPEVIQSLFVSETCDTYSYGVVLEWMLTREVFPFKGLEGLQVAVLWVVEKNERLTIPSS 230
QY 801 VNPKLASLIVACWADEPKRPFSSIMETLKPMT 834
DB 231 CPRSFAELLHQCEADAKKRPSPFKQIISILESMS 264

RESULT 6
US-10-440-341-7
* Sequence 7, Application US/10440341
* Publication No. US20030181413A1
* GENERAL INFORMATION:
* APPLICANT: RAPP, ULF

APP. HARALD
STORM, STEPHEN M.
TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVE., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/440,341
FILING DATE: 15-May-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/748,931
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683/82731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-440-341-7

Query Match 10.5%; Score 467.5; DB 12; Length 650;
Best Local Similarity 31.0%; Pred. No. 4.9e-30;
Matches 140; Conservative 80; Mismatches 166; Indels 65; Gaps 17;
QY 419 SLAKQYFLDSQSLNLFVDEASGNVSVGKDAAFSV-YORPLNRKDVQDKTIIVVTGDKORN 477
DB 190 SLAETALTSGSSPASDSIGQILTSFSPSKSIPIQPFPPADEDHNRN--QFGQDRS 247
QY 478 SOLNKKAAQLNTQDG-----KSEQFRSCVAGSYVQSTP-----FVENVVL----- 520
DB 248 SSAPN---VHINTIEPVNIDDLIRQDQGRGDSITGLSATPPASLPGLSLTNVKALQKSP 304
QY 521 ----SHISHIGSEDSHELLALSHPRMDHVNLPFVHGSQILRKPNELSLGLEDLVIPTWD 576
DB 305 GPQREKSSSSSDRNMKTGL--RRD-----SSDDWEIPDQ 340
QY 577 LDRREKIGAGSGFTVYRGEGWHSQDVAVKILTEQDHPERVNEFLREVAIMKSLRHPNVL 636
DB 341 ITVGQIRIGSGSGFTVYRGKWHG-DVAVKMLNLTAPTQQLQAFKNEVGLKTRHVNILL 399
QY 637 FMGAVTKPNNLSIVTEYLSRGLVRLHKGVDIDETRRINNAFDVAKGMNVLHRRDPP 696
DB 400 FMGYSTK-PQLAIVTQWCGSSSLYHLLHIIETK-FEMIKLIDIRQTACQMDYLHAKS-- 455
QY 697 IVHRDLKSNLLVDDKYTVKVCDFGLSRLKARTFLSS--KSAAGTPEWMAPEVLDRDEPSN 754
DB 456 IHRDLKSNLLVDDKYTVKVCDFGLSRLKARTFLSS--KSAAGTPEWMAPEVLDRDEPSN 754
QY 755 E---KSDVYSFGVILWELATLQPCWNLNPA-OVVAAV--GFKGKRLDIPRDVNPX-LAS 807
DB 516 PYSFQSDVYAFGIVLYELMTQQLPYSINNRDQIIFMVGRGYLSPDL SKVRSNCPKAMKR 575

QY 808 LIVACWADEPWKRPSFSSIMETLKPMTKQAP 838
DB 576 LMAECLKKRDERPLFPQILASIELLARS 606

RESULT 7

US-10-376-564-8
Sequence 8, Application US/10376564
Publication No. US20030180302A1
GENERAL INFORMATION:
APPLICANT: Wolf, Eckhard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the diagnosis or treatment of skin disorders and wound
TITLE OF INVENTION: Healing and for the identification of pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014003
CURRENT APPLICATION NUMBER: US/10/376,564
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 09/886,319
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
US-10-376-564-8

Query Match 10.5%; Score 467.5; DB 12; Length 765;
Best Local Similarity 31.0%; Pred. No. 6.3e-30;
Matches 140; Conservative 80; Mismatches 166; Indels 65; Gaps 17;
QY 419 SLAKQYFLDSQSLNLFVDEASGNVSVGKDAAFSV-YORPLNRKDVQDKTIIVVTGDKORN 477
DB 305 SLAETALTSGSSPASDSIGQILTSFSPSKSIPIQPFPPADEDHNRN--QFGQDRS 362
QY 478 SOLNKKAAQLNTQDG-----KSEQFRSCVAGSYVQSTP-----FVENVVL----- 520
DB 363 SSAPN---VHINTIEPVNIDDLIRQDQGRGDSITGLSATPPASLPGLSLTNVKALQKSP 419
QY 521 ----SHISHIGSEDSHELLALSHPRMDHVNLPFVHGSQILRKPNELSLGLEDLVIPTWD 576
DB 420 GPQREKSSSSSDRNMKTGL--RRD-----SSDDWEIPDQ 455
QY 577 LDRREKIGAGSGFTVYRGEGWHSQDVAVKILTEQDHPERVNEFLREVAIMKSLRHPNVL 636
DB 456 ITVGQIRIGSGSGFTVYRGKWHG-DVAVKMLNLTAPTQQLQAFKNEVGLKTRHVNILL 514
QY 637 FMGAVTKPNNLSIVTEYLSRGLVRLHKGVDIDETRRINNAFDVAKGMNVLHRRDPP 696
DB 515 FMGYSTK-PQLAIVTQWCGSSSLYHLLHIIETK-FEMIKLIDIRQTACQMDYLHAKS-- 570
QY 697 IVHRDLKSNLLVDDKYTVKVCDFGLSRLKARTFLSS--KSAAGTPEWMAPEVLDRDEPSN 754
DB 571 IHRDLKSNLLVDDKYTVKVCDFGLSRLKARTFLSS--KSAAGTPEWMAPEVLDRDEPSN 754
QY 755 E---KSDVYSFGVILWELATLQPCWNLNPA-OVVAAV--GFKGKRLDIPRDVNPX-LAS 807
DB 631 PYSFQSDVYAFGIVLYELMTQQLPYSINNRDQIIFMVGRGYLSPDL SKVRSNCPKAMKR 690
QY 808 LIVACWADEPWKRPSFSSIMETLKPMTKQAP 838
DB 691 LMAECLKKRDERPLFPQILASIELLARS 721

```
RESULT 8
US-10-376-564-7
; Sequence 7, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149,5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-376-564-7

Query Match          10.4%; Score 450; DB 12; Length 659;
Best Local Similarity 39.3%; Pred. No. 2.1e-29;
Matches 110; Conservative 59; Mismatches 97; Indels 14; Gaps 9;

QY 568 EDIVPTDLDREKIGAGSFGTVYRGWGHGSDVAVKILTEQDFHPRVNEFFREVAIMK 627
DB 341 DDWEIPDQITVGQIGSSGFGTVYKGRWHG-DVAVKMLNVTAPTQLOAQKNEVGVL 399
QY 628 SLRHPNIVLFMGAVTKPPNLSIVTEYLSRGLYRLHKSQKIDETIRINMADVAKGM 687
DB 400 KTRHVNILFMGYSTR-PQLAIVTQWCGSSLYHHLHIIETK-FEMIKLIDIASQTACGM 457
QY 688 NYLHRDPPITVHRDLKSPNLLVDKYYTVKVCDFGLSRKARTFLSS--KSAAGTPENWAP 745
DB 458 DYLHAKS--LIHRDLKSNILFHEDLTVKIGDFGLATVKRSWGSQHQEQLSGSILWAP 515
QY 746 EVLRDEPSNE---KSDVYSGFVILWELATLQOPWNCNMPA-QVVAV--GPKGKRLDIPR 799
DB 516 EVIRMDQKNPYSQSDVYAFGIVLYELMTGQLFYSNINNRDQIIFMVGKGYLSPDLKVR 575
QY 800 DVNPK-LASLIVACWADEPKWRPSSIMETLKPWKQAP 838
DB 576 SNCPKAKRLMABCLKKKDERPLFPQILASIELLARSIP 615

RESULT 9
US-09-828-313-29
; Sequence 29, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 18313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-29

Query Match          10.3%; Score 457.5; DB 9; Length 425;
Best Local Similarity 31.3%; Pred. No. 1.8e-29;
Matches 128; Conservative 73; Mismatches 139; Indels 69; Gaps 14;

QY 456 RPLARKVDGKTIIVTGDKNRSQ-----LNKKAQAQINTQD--CKSEQFR 499
DB 27 RTILKKD---KQLVNAADYDKRTPLHTAASLDCVPVAKVLLAEGAEINAKDRWKSPRGE 83
QY 500 SCVASPSYVQSTPFVENVVPLSHI---SHIGSEDSHELLALSHPRMDHVNNL-----PFV 551
DB 84 A-----ESAGYMNWVKLLKDYGAESHAGA-----PR-CHVESLIQVAPPLP 123
QY 552 HGSQIRKPNELSLGLEDLVIPWTDLDLREKIGAGSFGTVYRGWGHGSDVAVKILTEQDF 611
DB 124 SNRDWEIAPSEI-----ELDTSELIGKAGFEIRKALMRGTVPVAKTI-RPSL 170
QY 612 HPER--VNEERLEVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGLYRLHKSQVK 669
DB 171 SNDRWIKDFQHEVQLLVKVRHPNIVQFAGVTRQRPMLVTEFLAGDLHQLLRN--P 228
QY 670 DIDETRINMAFDVAKGNVYLRHRRDPPIVHRDLKSPNLLVDKYYTVKVCDFGLSRL---- 725
DB 229 NLAPDRIVKYALDIARGMSVYLNRSKPIIHRDLKPRNIIIVDEBELKVGDFGLSKLIDVK 288
QY 726 KARITLSSKSAAGTPENWAPVLRDEPSNEKSDVYSGFVILWELATLQOPWNCNMPAQVV 785
DB 289 LMHDVYKWTGTGSTRMAPEVFEHQYDKSDVDFSGMILYEMFEGVAPFEDKDAYDAA 348
QY 786 RAVGFKGKRLDI-PRDVNPKLASLIVACWADEPKWRPSSIMETLKP 833
DB 349 TLVARDKRPENRAQTPYPMQKALIEDCWSPYTPKRPFPFVEIVKLEVM 397

RESULT 10
US-09-513-145-6
; Sequence 6, Application US/09513145
; Publication No. US20020192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematosus and Diagnostic
; TITLE OF INVENTION: Assay
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-145-6

Query Match          10.3%; Score 457.5; DB 10; Length 648;
Best Local Similarity 35.3%; Pred. No. 3.3e-29;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;

QY 503 ASFPYSQSTPFVENVVPLSHISHIGSEDSHELLALSHPRMDHVNNLFFVHGSQILRKPE 562
DB 288 ASFSALSSSP-----NNLSPTGWSQPKTFVPAQREAP-----VSGTQ--EKNKI 330
QY 563 LSLGLEDLVPM-----TOLDLREKIGAGSFGTVYRGWGHGSDVAVKILTEQDFPPEVNE 618
DB 331 RPRGORDSSYYWEIEASEVMLSTRIGSGSFGTVYKGRWHG-DVAVKILKVVDPPTPEQFA 389
```

QY	619	FLREVAIMKSLRHPNIVLFWGAVTKPNNLSIVTEYLSRGLYRLHLKSGVZDIDETR---	675
DB	390	FRNEVAVLKTRHVNILLFPGYMTK-DNLAIYVTCWCEGSSLYKHLH-----	442
QY	676	--RINNAFDVAKGMNYLHRRDPPIVHRDLKSNLLVDKXYTKVCDPGLSLRLKARTFLSS	733
DB	443	FQOLIDIARQTAQGM DYLHAKN--IIHRDMKSNFIHLHEGLTVKIGDFGLATVKSRWSGSQ	500
QY	734	--KSAAGTPPEWMAPEVLR---DEPSNEKSDVYSGVILWELATLQOPWCNLPNA-QVVAA	787
DB	501	QVEQPTGTVLWMAPEVIRQDNPPFSQSDVYSYGIVLYELMTGLPYSHINNRDQIIFM	560
QY	788	VGFKRGKELDIPRDNV--PKLASLIVA-CWADEPFWKRPSPSSIMETLKPMTKQAP	838
DB	561	VGRGYASPDLSKLYKNCPKAMKELVADCVKVKKEBERPLFPQILSSIELLOHSLP	614
RESULT 11			
US-10-440-341-3			
; Sequence 3, Application US/10440341			
; Publication No. US20030181413A1			
GENERAL INFORMATION:			
; APPLICANT: RAPP, ULF			
; APP: HARALD			
; STORM, STEPHEN M.			
TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS			
NUMBER OF SEQUENCES: 8			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: CUSHMAN, DARRY & CUSHMAN			
STREET: 1100 NEW YORK AVE., N.W.			
CITY: WASHINGTON			
STATE: D.C.			
COUNTRY: USA			
ZIP: 20005			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/10/440,341			
FILING DATE: 15-May-2003			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 07/748,931			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			
NAME: SCOTT, WATSON T.			
REGISTRATION NUMBER: 26,581			
REFERENCE/DOCKET NUMBER: 5683/82731			
TELEPHONE: 202-861-3067			
TELEFAX: 202-822-0944			
TELEX: 6714627 CUSH			
INFORMATION FOR SEQ ID NO: 3:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 648 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: peptide			
SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
US-10-440-341-3			
Query Match 10.3%; Score 457.5; DB 12; Length 648;			
Best Local Similarity 35.3%; Pred. No. 3.3e-29;			
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;			
QY	503	ASPSYVQSTPTFVENVPLSHIGHSEHLLALSHPRMDHVNLPFVHGSQILRKPNKNE	562
DB	288	ASPSALSSSP-----NNLSPTGWSQPKTPVPAQRERAP-----VSGTQ--EKNGI	330
RESULT 12			
US-10-059-585-38			
; Sequence 38, Application US/10059585			
; Publication No. US20030082776A1			
GENERAL INFORMATION:			
; APPLICANT: Ota, Toshio			
; APPLICANT: Isogai, Takao			
; APPLICANT: Nishikawa, Tetsuo			
; APPLICANT: Hayashi, Koji			
; APPLICANT: Otsuka, Kaoru			
; APPLICANT: Yamamoto, Jun-ichi			
; APPLICANT: Ishii, Shizuko			
; APPLICANT: Sugiyama, Tomoyasu			
; APPLICANT: Wakamatsu, Ai			
; APPLICANT: Nagai, Keiichi			
; APPLICANT: Otsuki, Tetsuji			
; APPLICANT: Funahashi, Shin-Ichi			
; APPLICANT: Senoo, Chiaki			
; APPLICANT: Nezu, Jun-ichi			
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN			
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE			
FILE REFERENCE: 06501-098001			
CURRENT APPLICATION NUMBER: US/10/059,585			
PRIOR FILING DATE: 2002-01-29			
PRIOR APPLICATION NUMBER: PCT/JP00/05060			
PRIOR FILING DATE: 2000-07-28			
PRIOR APPLICATION NUMBER: US 60/183,322			
PRIOR FILING DATE: 2000-02-17			
PRIOR APPLICATION NUMBER: US 60/159,590			
PRIOR FILING DATE: 1999-10-18			
PRIOR APPLICATION NUMBER: JP 2000-118776			
PRIOR FILING DATE: 2000-01-11			
PRIOR APPLICATION NUMBER: JP 2000-183767			
PRIOR FILING DATE: 2000-05-02			
PRIOR APPLICATION NUMBER: JP 11-248036			
PRIOR FILING DATE: 1999-07-29			
NUMBER OF SEQ ID NOS: 64			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 38			
LENGTH: 648			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-059-585-38			
Query Match 10.3%; Score 457.5; DB 15; Length 648;			
Best Local Similarity 35.3%; Pred. No. 3.3e-29;			
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;			
QY	503	ASPSYVQSTPTFVENVPLSHIGHSEHLLALSHPRMDHVNLPFVHGSQILRKPNKNE	562
DB	288	ASPSALSSSP-----NNLSPTGWSQPKTPVPAQRERAP-----VSGTQ--EKNKI	330

[illegible]

RESULT 13

```

US-09-840-704-6
; Sequence 6, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
; APPLICANT: Dednar, Shoukat
; APPLICANT: Haunigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/840,704
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 271
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(271)
; US-09-840-704-6

```

Query Match	10.3%;	Score 456;	DB 10;	Length 271;
Best Local Similarity	39.5%;	Fred. No. 1.2e-29;		
Matches 109;	Conservative 58;	Mismatches 95;	Indels 14;	Gaps 9;
<p>572 IPTWDLREKIGAGSFGTVYRGWGHGSDVAVKILTEQDFHPERVNEFLREVAIMKSLRH 631</p> <p> :</p> <p>Db 1 IPDGOITVGQIRIGSGSGFTVYKGVKHG-DVAVKMLNVTAPTQOLQAFKNEVGLVKTRH 59</p>				
QY	632	PNIVLFMGNAVTKPPNLSGVTVYLSRGSILYRLKLSGVKQIDETFRINMAFDVAKGMVYLH 691		
Db	60	VNILLFMGVSTK-PQLAIVTQWCGSSLYHHLIETK-FEMTKLIDIAQRTAQGMVYLH 117		
QY	692	RRDPFTVHRDLKSPNLLYDKYTVYKVCDFGLSRLLKARTFLSS--KSAAGTPEWMAPEVLR 749		
Db	118	AKS--IIHRDLKSNNIIFLHEDLVKIGDFGLATYKSEWSGSHQFQLSGSILLWMAPEVIR 175		
QY	750	DEPSNE---KSDVYSGFVILWELATLQCPMCLNPA-QVVAAY--GFKKRLIDPRDVP 803		
Db	176	MDQKPYSPQSDVYAFGVILFELMTGQLPYSNINNRDQIIFMVGKRGYLPDLSKYRNCNP 235		
QY	804	K-LASLIVACNADEPKWKPFSSTMETLKPMTKOAP 838		
Db	236	KAMKRLMARCLAKKXDRDEPLPQIILASTELLARSLP 271		

RESULT 14

```

US-09-976-782-40
; Sequence 40, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grossee et al
; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Consensus
; OTHER INFORMATION: sequence
US-09-976-782-40

```

RESULT 15

```

RES001 13
US-09-976-782-29
; Sequence 29: Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1
; FILE REFERENCE: 21402-157

```


Sat Oct 25 11:01:51 2003

```
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Consensus
; OTHER INFORMATION: sequence
US-09-976-782-29

Query Match          10.3%; Score 455; DB 12; Length 257;
Best Local Similarity 40.0%; Pred. No. 1.3e-23;
Matches 104; Conservative 50; Mismatches 94; Indels 12; Gaps 7;

QY 579 LREKICAGSFGTVYRGWHGS-----DVAVKILTEQDPFHPERVNEFLREVAINMKSRLRHPN 633
Db 2 LGKLGEGAFGEVYKGTLLKGKGVVEVAVKTLKE-DASEQQIEEFLREARLRKLDHPN 60
QY 634 IVLFMGAVTKPNLSIVTEYLSRGSLYLLHKSGVKDIDETRRINMAFDVAKGMVYLHRR 693
Db 61 IVKLLGVCTEEEPMLIVMEYMEGGDLDDLRLRNRPKELSLDLSLQALQARGWEVLESK 120
QY 694 DPPIVHRDLKSNLIVDKKTYTKVCDPGLSLR-LKARTFLSSKSAAGTP-EMWAPVLRDE 751
Db 121 N-FVHRDLAARCLVGENKTVKIADFGIARDLYDDDYRKKKSPRLPIRWAPESLKOG 178
QY 752 PSNEKSDVYSFGVILWELATL-QQPCWNLNPAQVVAAGVFGKBLDIPROVNPKLASLIV 810
Db 179 KFTSKSDVWSFGVLLWEIIFTLGESYPGNSNEEVLEYLK-KGYRLPQPPNCPDEIYDML 237
QY 811 ACWADSPMKRPSFSSIMETL 830
Db 238 QCWADPEDEPTFSELVERL 257
```

Search completed: October 23, 2003, 17:30:39
Job time : 42 secs

1348 CCAAGACTAAACCTATTGTAATCTACATTGATTTCCAGTCTAGTCCCAACAGATTATTC 1407
1417 CCACGACCAAGCCAGTTGAACCGCAGTCGATTTTGTAGTTACTAGCCCAACAATATTC 1476
1408 TTGGATAGCCAAATACATTAATCTTGTATTTGATGAAGCTTCTTCAGGTAAATGTTGTATCT 1467
1477 TCCGATAGCCAGTCTCTTAATCTTGTATTTGATTCGATCTAG----- 1519
1468 GGAAGGATGCTGATCTCTCGTCTATCAAGGCCATTAATAAGGAGATGATAGGA 1527
1520 ----ATGATATGGGATCTCAATGTTTCTATAGCAATATGATAATCCGGGTGGAGAGAT 1575
1528 ABAACCATAGTGGTTACTGTGACAGGACAGAAATCTCAGTTATTAATAAATAAGCA 1587
1576 GACGATTTGGCAAAAATGGTG----- 1597
1588 GCCCAACTGAATACTCAAGATGGAAAGCTGTAGCAAAATTTAGATCATGTGTTGCTCTTCCA 1647
1598 ----- 1597
1648 TATAGTGTACAGTCGACCCCTTTTGTAGAAATGTAGTCCCTTTAAGCCATATCTCACAC 1707
1598 -----GTGGGTCTTTGGCACCC 1614
1708 ATTGGTCTTGAAGATTGGAGCATCTCTTAGCATTTGTCATCCAAAGGATGGATCATGTT 1767
1615 AGTGCTAATATGCTCCACAGACATGATGCTGCGTCAAAATCAAAATTTGAAGCAGCACCT 1674
1768 AACAAATTTACATTTGTCATGCTAGTGTGATGTTAGAAAACCAATGAGCTTTCCCTT 1827
1675 ATGAATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGCAATAGGAACTTGGACTT 1734
1828 GCTTTAGAAAGATTTGGTTATTTCCATGGACAGATCTTGATTTGAGGGAGAAAATTTGAGCA 1887
1735 GATGCTGATGATGAGACATCCCGTGTGTGATCTTAATATAAAGAAAAGATTTGGAGCA 1794
1888 GGTCTTTTGGAGCTGTATATCGTGGTGGAGTGGCTCTGATGTTGCTGTGAGATC 1947
1795 GGTCTCTTGGCACTGTCCACCGTCTGAGTGGCATGGCTCGGATGTTGCTGTGAAAAT 1854
1948 CTCACAGAACAGACTTCCATCTCTGAAGCTGTTAATGAGTTTCTGAGAGAGTTGCTATC 2007
1855 CTCATGGAGCAAGACTTCCATCTGAGCGTGTAAATGAGTTCTTAAGAGAGTTGGGATA 1914
2008 ATGAATCTTTAGCATCTCAATATTTGATGTTTATGGTGGGTGACCAAGCCACCA 2067
1915 ATGAAGCGCTTTCGCCACCTAACATTTCTCTTCATGGTGGGTCACTCAACCTCCA 1974
2068 AACTTGTCCATTGTCAACCAATATCTATCGAGAGTAGCTTTGTATAGGCTTTTGCATAAG 2127
1975 AATTGTCAATAGTACAGAAATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAA 2034
2128 TCAGGTGTCA---AAGACATAGATGAACACGTCGAATAAATATGGCTTTTGTATGGCA 2184
2035 AGTGGAGCAAGGAGCAATTAGATGAGAGACGTGCGCTGAGTATGGCTTATGATGTGGCT 2094
2185 AAGGGATGAATCTACTCTCCACAGAGTGTATCTCCAAATTTGTCGTGATTTAAATATCA 2244
2095 AAGGGATGAATATCTTCCAAATGCAATCTCCAAATTTGTCATAGATGATCAATCT 2154
2245 CCGAATCTGTTAGTGTACAGAGATATACAGTCAAGTTTGTGATTTGGTCTCTCCCGT 2304
2155 CCAAACTTATTTGGTTCACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCCGA 2214
2305 TTAAGGCGCACATTTCTTTCATCCAAATCTGAGCTGGAACACCTGAATGGATGGCA 2364
2215 TTGAAGCCAGACGTTTCTTCTCTGAAAGTACAGAGCTGGACCCCGAGTGGATGGCA 2274
2365 CCAGAAAGTACTACCGCATGAACCAATCAAAATGAATAAGTACAGATGTTTACAGTTTGGAGTG 2424
2275 CCAGAAAGTCTCGAGATGAGCGGTCTAATGAAGAAGTACAGATGTGTACAGCTTCCGGGTC 2334
2425 ATTTTGGGAGTGTGCAACTTTTGGCAACGCCATGCTGTAACTAAACCCAGCTCAGGTT 2484

2335 ATCTTGTGGAGCTTGTCTACATTCGACACCATGGGTAACTTAATCCGGCTCAGTT 2394
2485 GTGCGAGCTGTTTGGATTTAAGGGCAAAAAGGCTTGACATCCCACTGATGATTAATCCCAAA 2544
2395 GTAGCTGCGGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGCGTAAATCTGAATCCTCAG 2454
2545 TTGGCTTCTTAAATAGTCTTGTGCGCCGATGAGCCATGGAACACGTCCTCTCTTTTCC 2604
2455 GTTGCAGCCATTAATGAGGTTTGTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCA 2514
2605 AGCATTATGAAACCTTGAACCAATGACTAAACAAAGCGCCACCTCAACAAAGTGGCA 2664
2515 ACTAATAGACTTGTCTAAGACCAATGATCAAAATCAGCGGTTCTCTCCGCCAACCGCTCG 2574
2665 GA 2666
2575 GA 2576

RESULT 3
US-08-003-311B-1
; Sequence 1, Application US/08003311B
; Patent No. 544166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kiebel, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 544166r18
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
; US-08-003-311B-1

Query Match 27.4%; Score 898.8; DB 1; Length 3033;
Best Local Similarity 64.3%; Pred. No. 5.7e-227;
Matches 1582; Conservative 0; Mismatches 664; Indels 216; Gaps 7;

Qy 253 AAGGGAGAACCGATAGGCTTTTGAATGGGATGGGAGTGGTGATCAACAGGTTAAACAG 312
Db 283 AGAGGCGGATTTGATTTGGGATCTAGCGGTGGTGGTGATCATAGGTGAATAAT 342
Qy 313 CAGGCGTATCGGATAGGAGACCTGT-----ATTCAATGGATTGGTTTACAGAGACATTC 366
Db 343 CAACCGAATCGGTTGGGAATAATATGATGCTTCTCTAGGGTTGCAAGGCAATCC 402
Qy 367 AGTGAAGCAGCTACGATGATAGTCTCTCTCTAGTATCTACTACGCAACGACGCTATCA 426
Db 403 AGTGGAGTAGTTTCGGTGAGAGCTCTTGTCTGGGATATATACATGCTACGCTACGCTTTC- 461
Qy 427 AACCTTCACCAATGATCAATGATGATGATGATATATCTCGATGATGATTTCCGAGTG 486
Db 462 -TGCGGCGCTAACGAGATCGAATCTGTGGATTTCTCAAGATGATGGTTTAGGCTT 519
Qy 487 ATGAAGCTGTGGAAAGTGAGAGTTCG----- 513
Db 520 GGATTTGGTGGTGGAGAGATTTGAGGATACAGATGGCGGAGCTCCCGTGGAGG 579
Qy 514 -----TCTGGAAGACTGGGCCAGCAGACGGAAGAGCTTTTCAGTTGCGAGAGCC 567
Db 580 TCTTCATCTGGGAAGACTGGGCCAGCAGACGGAAGAGTATCAGCTGCGAGTTGCA 639
Qy 568 TTGTTTCTTAGGCTTTCTTCAGATGNNACTTGTGCGGATGCCCACTTTATGATCCG 627
Db 640 TTGCGTTAAGGCTTTCTGCGAGGCTACTTGTGCGGAGATCCGAACCTTTCTGGATCCT 699
Qy 628 ATTCCAGCAGGAGGAGCTTTAAGATCGTTATCGATTTACAGTTGAGGCCATCTCGATCG 687
Db 700 GTACCGAGCAGTCTGTTTACGAGCTTCGCCAAGTTTCAGCCGAAACCGTTTCACTCGT 759
Qy 688 TTCTGGGTAAATGATGCATCTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAAT 747
Db 760 TTCTGGGTAAATGATGCATCTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAAT 819
Qy 748 CATGGGATGACCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807
Db 820 AATGGTCTGATCCCTATATTTGGACCTTATGATGATGATGATGATGATGATGATGATG 879
Qy 808 CCATCATTTGAATCTCGAAAAAGTGTATTTCCAGCATCGTTTCATCAATTCAGATGAT 867
Db 880 CCTTCATTTGAATCATTAAGAGCTGTGATCTGTGTTGATCTTCGCTTGAAGGATC 939
Qy 868 TTGATAGATCGGCATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 927
Db 940 ATAGTTGATAGCGTAGTATTCAGCCCTTCAGAGAACTTCACAAATAGATCCACGACATA 999
Qy 928 TCTTCCAGTGTGTAACCAAGAGGTTGAGATCATATAGCAAGCTGGTATGCAAT 987
Db 1000 TCTTGTAGCTGCATTCACCAAGAGGTTGTTGATCAGCTGGCAAGGTTATCTGCAAT 1059
Qy 988 CACTTGGGGGTTTCAGTTTCTGAGGAGAGATGACCTTGGTTCTGCTGGAGGAATGC 1047
Db 1060 CGTATGGGGGTCAGTTATCATGGGGAAGATGAGTTGGTTCCCATGTTGGAAGAGTGC 1119
Qy 1048 AGCGATGCTTAAAGGAATGTTGGGATCTGCTGATTCCTTATCCCTTATGAGCTTATCTGTT 1107
Db 1120 ATTGATGCTTAAAGGAATCTTTAAA---GTGGTGGTTCCCATAGGTAGCTCTCTGTT 1176
Qy 1108 GGCCTTTTGACATCTGCTCTTTTATTTCAAGTCTCTAGCTGATTCATTTGATTTTACCC 1167
Db 1177 GGACTCTCAGACATCGAGCTTTACTCTTCAAGTACTGCTGACATATTTGATTTACCC 1236
Qy 1168 TGTGAAATGCAAGGATGTAATATTTGACATGAGATGATGCTTCATCTTGCCTTGT 1227
Db 1237 TGTGAAATGCAAGGATGTAATATTTGTAATAGACATGCTGCTGCTGCTGCTGCTGCTG 1296
Qy 1228 AGGTTGGGCTGTATAGGAAATCTCTCATGATCTGATTTGGGAGGCGAGGCTCTTATGCT 1287
Db 1297 AGGTTGGGCTGTATAGGAGTACTGTTGATTTAGTAGGAAGCAGCTCACTTATG 1356
Qy 1288 CAACCTGATCTCTTGGCTCAATGGTGCATCATCCATCTCAATTTCTTCACCATTTGGATTT 1347

Db 1357 GAGCCTGATCTCTGCTAAATGGTCCCTTCATCTATCTCAATTTCTCTCTCTCGGTTT 1416
Qy 1348 CCAAGCTAAACCTATTTGAATCTACCAATTCAGTTTCAGGTCACTGGCCAAACAGATTTTC 1407
Db 1417 CCAGGACCAAGCCAGTTTGAACCCGACGTGATTTAGGTACTAGCCAAACAATAATTTTC 1476
Qy 1408 TTGGATAGCCAACTCACTTAATCTTGTATTTGATGAAGCTCTTCAGGTAAATGTTGTATCT 1467
Db 1477 TCCGATAGCCAGTCTCTTAATCTTGTATTTTCGATCCTGCAATCAG----- 1519
Qy 1468 GGGAAAGGATGCTGCAATTTCTCGCTCTATCAAAAGGCCATTAAATAGGAAGGATGTAGATGA 1527
Db 1520 ----ATGATATGGATTTCTCAATGTTTCATAGGCAATATGATTAATCCGGGTGGAGAGAT 1575
Qy 1528 AAAACCAATAGTGGTTACTTGGTGAAGGACAGAAATCTCAGTTATTAAATAAAGCA 1587
Db 1576 GACGCATTGGCAGAAATAGGTG----- 1597
Qy 1588 GCCMACTGAATACTCAAGATGGAAAGTCTGAGCAATTTAGATCATGTGTTGTTCTCCA 1647
Db 1598 ----- 1597
Qy 1648 TATAGTGTACGTGACGCCCTTTTGTAGAAATATGATGCCCTTTAAGCCATATCTCACAC 1707
Db 1598 -----GTGGGTCTTTGCCACC 1614
Qy 1708 ATTGGTTCTGAAGATTGGAGCATCTCTAGCATTTGTCTCATCAAGGATGGATCATGTT 1767
Db 1615 AGTGTAAATATGCTTCCACAGAACATGATGGTGGTCAATCAATTAATGAAGCAGCACCT 1674
Qy 1768 AACAAATTTACATTTGTTTCATGTTAGTGTGATGTAGAAACCAATAGACTTTCCCTT 1827
Db 1675 ATGAATGCCCCCAATCAGTCAGCCAGTTCCAAACAGGGCAAAATAGGAAATCTTGGACTT 1734
Qy 1828 GGCTTAGAAGATTTGGTTATTCATGGAAGATCTTGTATTTGAGGAGAAATAGGAGCA 1887
Db 1735 GATGTTGATGATGAGCATCCGTTGGTGTGATCTTATATAAAGAAAGATGGAGCA 1794
Qy 1888 GPTTCTTTTGGAGCTGTATATCGTGGTGGAGTGGCATGGCTCTGATGTTGCTGTGAAGATC 1947
Db 1795 GPTTCTTTTGGAGCTGTATATCGTGGTGGAGTGGCATGGCTCTGATGTTGCTGTGAAGAT 1854
Qy 1948 CTCACAGAACAGACTTCCATCTCGAAGTGTATGATGATTTCTGAGAGAGGTTGCTATC 2007
Db 1855 CTATGGAGCAAGACTTCCATCTGAGCGTGTATGAGTTCTTAAGAGAGGTTGCGATA 1914
Qy 2008 ATGAAATCTTTACGACATCTTAATATTTGATGTTTATGGTGGGTTGACCAAGCCACA 2067
Db 1915 ATGAAAGCCTTGGCCACCCTAACATTTGTTCTTCTTCATGGGTGGGTCACTCAACCTCCA 1974
Qy 2068 AACTTGTCCATTTGTCACCGAATATCTATCGAGAGGATGTTGATAGGCTTTTGCATAAG 2127
Db 1975 AATTTGTCAATAGTACAGAAATTTTGTCAAGAGTATTTTATACAGACTTTTTCATAAA 2034
Qy 2128 TCAGTGTGTC---AAGACATAGATGAAACACGCTCGAATAAATATGGCTTTTGTATGTCGA 2184
Db 2035 AGTGGAGCAAGGAGCAATTAGATGAGAGACGCTCGCTGAGTATGGCTTATGATGTGCT 2094
Qy 2185 AAGGAATGAACTTACCTCCACAGAGTGTATCTCCAATTTGTTTCATCGTGAATTTAAATCA 2244
Db 2095 AAGGAATGAAATATCTTCCAAATCGCAATCTCCAATTTGTCATAGAGATCTAAAATCT 2154
Qy 2245 CCGAATCTGTTAGTGTGCAAGAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCGCT 2304
Db 2155 CCAACTTATTTGTTGCAAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGGA 2214
Qy 2305 TTAAGGCAAGCAATTTCTTTTCATCCAAATCTGAGCTGGAAACACCTGAATGGATGCA 2364
Db 2215 TTGAAGCCAGCAGCTTTCTTCTCCTGAAAGTCAAGCTGGAAACCCCGAGTGGATGCA 2274
Qy 2365 CCAGAGTACTTACCGATGAACCATCAATGAAATGAAAGTCAAGTGTATTACAGCTTTGAGTGT 2424

Db 2275 CCAGAACTCTCGAGATGAGCGCTTAATGAAAAAGTCAGATGTGTACAGCTTTCGGGTC 2334
Qy 2425 ATTTTGGGGAGTTGGCAACTTTTGCACAGCCATGTTGAATCTAAACCCAGCTCAGGTT 2484
Db 2335 ATCTTGGGAGCTTGCTACATTTGCACAAACACATGGGGTAATTAATCCGGCTCAGGTT 2394
Qy 2485 GTCCGAGCTGTGTGANTTAAGGGCAAAAGGCTTTGACATCCCAAGCTGATGTAATCCCAA 2544
Db 2395 GTAGCTGGGTTGGTTTCAAGAGTAAACCGCTGGAGATCCCGGTAATCTGAATCCTCAG 2454
Qy 2545 TTGGCTTCTTAATAGTGGCTTGTCTGGCCGATGAGCCATGAAACGCTCTCTTTTCC 2604
Db 2455 GTTGCAGCCATAATCGAGGTTGTGGACCAATGAGCCATGAAAGCTTCATATTGCA 2514
Qy 2605 AGCAATTATGAAACCTTGAACCAATGATTAACAAGAGCCCACTCAACAAGTGGACA 2664
Db 2515 ACTATAATGGACTTGTCTAAGACCATTTGATCAATCAGCGGTTCTCCGCCCAACCGCTCG 2574
Qy 2665 GA 2666
Db 2575 GA 2576

RESULT 4

US-08-261-432-1
; Sequence 1, Application US/08261432
; Patent No. 5602322
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5602322ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,432
; FILING DATE: June 17, 1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/003,311
; FILING DATE: January 12, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
US-08-261-432-1

Query Match

27.4%; Score 898.8; DB 1; Length 3033;

Best Local Similarity 64.3%; Pred. No. 5.7e-227;
Matches 1582; Conservative 0; Mismatches 664; Indels 216; Gaps 7;
Qy 253 AAAGGAGAACCATAGAGGTTTGTGATGGGATGGGATGGGATGATCAGAGTTAAACAG 312
Db 283 AGAGCGGATTTGATTTGGGATCCTAGCGTGGTGGTGGTGGTATCATAGGTTGAATAA 342
Qy 313 CAGCGTATCGGATAGGGAACCTGT-----ATTCAATGATTTGGTTTACAGAGACATTC 366
Db 343 CAACCGAATCGGTTGGGATATATGATGCTTCTCTAGGTTGCAAGGAATTC 402
Qy 367 AGTGAAGCAGCTACGATGATAGCTCTCTCTAGTATGATTAATCAGCAGCCAGGATCA 426
Db 403 AGTGGAGTATTTCTGGTGGAGCTCTTTGTCTGGGGATTAATACATCCTACGCTTTC- 461
Qy 427 AACCTCAGCAATAGATCAATGCAATGCAATGCAATATATCTCGATGATGATTTCCGAGTG 486
Db 462 --TGGCGGCTAACGAGATCGAATCTGTTGGATTTCCTCAAGATGATGGTTTAGGCTT 519
Qy 487 ATGAAGCTGTGGAGTGGAGGTTCTG----- 513
Db 520 GGATTTGGTGGTGGAGGAGATTTGAGGATACAGATGGCGCGGATCTCCGCTGGAGGG 579
Qy 514 -----TCTGAAAGAGCTGGGCCAGCAGAGCGAGAGAGCTTTTCAGTTGCAGCAGCCC 567
Db 580 TCTTCACTCGGAAGAGCTGGGCGCAGCAGACGAGGAGATTAATCAGCTGCAGCTTGA 639
Qy 568 TTGGTTCTTAGGCTTCTTCAGATGNNACTTCTGGGATGATCCCAACTTTATGGATCG 627
Db 640 TTGGCTTAAGGCTTTCTCGAGGCTACTTTGCGGAGATCCGAATCTTCTGATCCT 699
Qy 628 ATCCAGACAGGAGCTTTAAGATCGTTATGATCTTTCAGTTTTCAGCTGAGGCCATCTCGCATCG 687
Db 700 GTACCGGACGAGTCTGCTTTACGACTTCGCCAAGTTCAAGCGAAACCGTTTCAATCGT 759
Qy 688 TCTGGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
Db 760 TCTGGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
Qy 748 CATGGATGACCCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
Db 820 AATGCTCTGGATCCCTATATTTGGACCTTATGACATCGACCTGCATGAAAGTGGTCGATC 879
Qy 808 CCATCATTTCAATCTCTGAAACAGTTGATTCAGCATCGGTTTCATCAATTTGAAGTAGTT 867
Db 880 CTTCAATTAATCATAGAGCTGTTGATTTGTTGATTTGTTGATTTGTTGATTTGTTGATTTG 939
Qy 868 TTGATAGATCGCATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 927
Db 940 ATAGTTGATAGGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
Qy 928 TCTTCCAGTTGTGTAAACCAAGAGGTTGAGATGATGATGATGATGATGATGATGATGATGAT 987
Db 1000 TCTTGTAGCTGCAATACCAAGAGGTTGTTGATGATGATGATGATGATGATGATGATGATGAT 1059
Qy 988 CACTTGGGGGTTCACTTTCTGAGGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1047
Db 1060 CGTATGGGGGCTCCAGTTATCATGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1119
Qy 1048 AGCATGATTAAGGAATGTTTGGGATCTGCTGTTGATTTCCCTTATGATGATGATGATGATGAT 1107
Db 1120 ATTGATGCTTAAAGAAATCTTTAA-----GTGGTGGTTTCCCATAGGATGATGATGATGAT 1176
Qy 1108 GGCCTTTGTAGATCGTCTCTTTTATTTCAAGTCTTAGCTGATTTCAATGATTTACCC 1167
Db 1177 GGAATCTGACAGATCGAGCTTTTACTCTTTCAAGTCTTAGCTGATTTCAATGATTTACCC 1236
Qy 1168 TGTGAAATGCCAAAGGATGATAATTTGCACTAGAGATGATGATGATGATGATGATGATGATGAT 1227
Db 1237 TGTGAAATGCCAAAGGATGATAATTTGTAATAGAGAGATGCGGCTTCTGCTGCTGTC 1296
Qy 1228 AGTTGGGCTTGTAGAGGAAATATCTCATGATCTGATTTGGAGGCGAGGTTGTTATGC 1287


```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-928-464-5

Query Match      4.7%; Score 155.2; DB 1; Length 5890;
Best Local Similarity 69.4; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY      693  GGTAAATGGATGCATGTCATATTGTGAGAAAGTGCCAGATGCTTTTATATCTAAATCTAATGG 752
      |||
Db      1176  GGTAAATGGCTGCTTCTCGTACTACTATGATAAAGTTCCTGATGGTTTATATATGATGAATGG 1235

QY      753  GATGAACCCATATGTATGGTCATTATGCAACAACTCTGAAAGAGATGGCGGTATACCATC 812
      |||
Db      1236  TCTGGATCCCTATATTTTGGACCTTTATGTCATCGACCTGTCATGAAGTGTGTCATCCCTTC 1295

QY      813  ATTTCAAATCTCTGAAACACAGTTGATTCACAGATCCGGTTTCATCAAATGAAGTAGTATTTGAT 872
      |||
Db      1296  AATTGAAATCATTAGAGCTGTGATTCCTGGTGTGATCTTTCGCTTGAAGCATCATAGT 1355

QY      873  AGATCGGCATAGTGATGCTAGCTTTAAAGAACTGCAAAAACAGGGTGCAATATATTTCTTC 932
      |||
Db      1356  TGTATAGGCGTATGATCCAGCGTTTCAAGAGAACTTCAATAGAGTCCAGCATATCTTG 1415

QY      933  CAGTTGTGTATACCCAAAGAAGGTTGCAGATCATATAGCAAAAGCTGGTATGCAATCACTT 992
      |||
Db      1416  TAGCTGTCATATTACCAAAAGAAGGTTGTGATCATAGCTGGCAAGGCTTATCTGCATCTGAT 1475

QY      993  GGGG 996
      |||
Db      1476  GGGG 1479

```

RESULT 9
 US-07-928-464-6
 ; Sequence 6, Application US/07928464
 ; Patent No. 5367065
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, Joseph R.
 ; APPLICANT: Kieber, Joseph J.
 ; TITLE OF INVENTION: Constitutive Triple Response Gene and
 ; TITLE OF INVENTION: Mutations
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
 ; ADDRESSEE: No. 5367065ris
 ; STREET: One Liberty place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/928,464
 ; FILING DATE: 19920810
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Miller, Suzanne E.
 ; REGISTRATION NUMBER: 32,279
 ; REFERENCE/DOCKET NUMBER: UPN-1086
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5890 base pairs

```

; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-928-464-6

Query Match          4.7%; Score 155.2; DB 1; Length 5890;
Best Local Similarity 69.4%; Pred. NO. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY      693  GGTTAAATGGATGCATGTCATATTGTTGAGAAAGTCGCAGATGGTTTTTATCTTAATTCATGG 752
Db      1176  GGTTAATGGCTGCTTATCGTACTATCATATAAGTTCCTGATGGTTTTTATATGATGAATGG 1235

QY      753  GATGACCCATATGATATGTTTCATATTGCACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db      1236  TGTGATCCCTTATATTGGACCTTTATGCACTGCACCTGCATGAAAGTGTGCGATCCCTTC 1295

QY      813  ATTTGAATCTCTGAAACACAGTTCATTCACAGCATCGGTTTCATCAATGAAGTAGTTTTGAT 872
Db      1296  AATTGAATCATATAAGAGCTCTTGATTCTCGTGTGTATTCTTCGTTTGAAGCGATCATAGT 1355

QY      873  AGATCGGCATAGTCATGCTAGCTTTAAAGAAGACTGCAGAAAACAGGGTGCATAATATTTCTTC 932
Db      1356  TGAATAGGGGTAGTAGTCCAGCCTTCAAGGAACCTTCACAAATAGAGTCCACGACATATCTTG 1415

QY      933  CAGTTGTGTATACCAACAAGAGGTTTCAGATCATATAGCAAGAGCTGGTATGCAATCACTT 992
Db      1416  TAGCTGCAATTACCAACAAGAGGTTTGTATTCAGCTGGCAAGAGCTTATCTGCAATCGTAT 1475

QY      993  GGGG 996
Db      1476  GGGG 1479

```

```

1 RESULT 10
2 PCT-US93-07347-3
3 ; Sequence 3, Application PC/TUS9307347
4 ; GENERAL INFORMATION:
5 ; APPLICANT: Ecker, Joseph R.
6 ; APPLICANT: Kieber, Joseph J.
7 ; TITLE OF INVENTION: Constitutive Triple Response Gene and
8 ; TITLE OF INVENTION: Mutations
9 ; NUMBER OF SEQUENCES: 6
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
12 ; ADDRESSEE: Norris
13 ; STREET: One Liberty Place - 46th Floor
14 ; CITY: Philadelphia
15 ; STATE: PA
16 ; COUNTRY: U.S.A.
17 ; ZIP: 19103
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: PCT/US93/07347
25 ; FILING DATE: 19930805
26 ; CLASSIFICATION:
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: Miller, Suzanne E.
29 ; REGISTRATION NUMBER: 32,279
30 ; REFERENCE/DOCKET NUMBER: UPN-1086
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: 215-568-3100
33 ; INFORMATION FOR SEQ ID NO: 3:
34 ; SEQUENCE CHARACTERISTICS:
35 ; LENGTH: 5690 base pairs
36 ; TYPE: nucleic acid
37 ; STRANDEDNESS: single
38 ; TOPOLOGY: linear

```

MOLECULE TYPE: DNA (genomic)
FEATURE: intron
NAME/KEY: 1.353
LOCATION: 1.353
FEATURE: exon
NAME/KEY: 354..1001
LOCATION: 354..1001
FEATURE: intron
NAME/KEY: 1002..1176
LOCATION: 1002..1176
FEATURE: exon
NAME/KEY: 1177..1477
LOCATION: 1177..1477
FEATURE: intron
NAME/KEY: 1478..1574
LOCATION: 1478..1574
FEATURE: exon
NAME/KEY: 1575..1719
LOCATION: 1575..1719
FEATURE: intron
NAME/KEY: 1720..1936
LOCATION: 1720..1936
FEATURE: exon
NAME/KEY: 1937..2038
LOCATION: 1937..2038
FEATURE: intron
NAME/KEY: 2039..2173
LOCATION: 2039..2173
FEATURE: exon
NAME/KEY: 2174..2379
LOCATION: 2174..2379
FEATURE: intron
NAME/KEY: 2380..2736
LOCATION: 2380..2736
FEATURE: exon
NAME/KEY: 2737..3012
LOCATION: 2737..3012
FEATURE: intron
NAME/KEY: 3013..3202
LOCATION: 3013..3202
FEATURE: exon
NAME/KEY: 3203..3243
LOCATION: 3203..3243
FEATURE: intron
NAME/KEY: 3244..3519
LOCATION: 3244..3519
FEATURE: exon
NAME/KEY: 3520..3588
LOCATION: 3520..3588
FEATURE: intron
NAME/KEY: 3589..3668
LOCATION: 3589..3668
FEATURE: exon
NAME/KEY: 3669..3769
LOCATION: 3669..3769
FEATURE: intron
NAME/KEY: 3770..3858
LOCATION: 3770..3858
FEATURE: exon
NAME/KEY: 3859..3943
LOCATION: 3859..3943
FEATURE: intron
NAME/KEY: 3944..4037
LOCATION: 3944..4037
FEATURE: exon
NAME/KEY: 4038..4136
LOCATION: 4038..4136
FEATURE: intron
NAME/KEY: 4137..4369
LOCATION: 4137..4369
FEATURE: exon
NAME/KEY: 4370..4438
LOCATION: 4370..4438

FEATURE: intron
NAME/KEY: 4439..4541
LOCATION: 4439..4541
FEATURE: exon
NAME/KEY: 4542..4673
LOCATION: 4542..4673
FEATURE: intron
NAME/KEY: 4674..4787
LOCATION: 4674..4787
FEATURE: exon
NAME/KEY: 4788..4882
LOCATION: 4788..4882
FEATURE: intron
NAME/KEY: 4883..4959
LOCATION: 4883..4959
FEATURE: exon
NAME/KEY: 4960..5056
LOCATION: 4960..5056
FEATURE: intron
NAME/KEY: 5057..5890
LOCATION: 5057..5890
PCT-US93-07347-3
Query Match 4.7%; Score 155.2; DB 5; Length 5890;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
Qy 693 GGTAAATGGATGATGTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1176 GGTTAATGGCTGTTATCGTACTATGATAAAGTTCCTGATGGTTTTTATATGATGAATGG 1235
Qy 753 GATGGACCATATGATGTCATTTATGACCAATCTGCAAGAGGATGGCGTATACCATC 812
Db 1236 TCTGGATCCCTATATTTGGACCTTATGATCGATCGATGAAAGTGTGCAATCCCTTC 1295
Qy 813 ATTTGAATCTCTGAAACAGTTGATTCAGCATCGGTTTCATCAATTTGAAGTAGTTTGTAT 872
Db 1296 AATTGAATCATTAAAGAGCTGTTGATTCGTTGATTCCTCGTTGAAGCATCATAGT 1355
Qy 873 AGATCGGCATAGTATGCTAGCTTAAAGAACTGCAAAACAGGTCATATATTTCTTC 932
Db 1356 TGATAGCGTAGTATGATCCAGCCCTTCAAGAACTTCACAAATAGATCCACGACATATCTTG 1415
Qy 933 CAGTTGTGTAAACACAAAGAGGTTTCAGATCATATAGCAAAAGCTGGTATGCAATCATT 992
Db 1416 TAGTCGATTACCAAAAGAGGTTGTTGATCAGTGGCAAGCTTAICTGCAATCGTAT 1475
Qy 993 GGGG 996
Db 1476 GGGG 1479

RESULT 11
PCT-US93-07347-5
Sequence 5, Application PC/TUS9307347
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07347
FILING DATE: 19930805
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-07347-5

Query Match 4.7%; Score 155.2; DB 5; Length 5890;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAATGGATGTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1176 GGTAAATGGCTGTTATCGTACTATGATAAAGTTCCTGATGGTTTTTATATGATGAATGG 1235
QY 753 GATGACCCATATGATGTCATATGACCAATCTGCAAGAGGATGGGCGTATACCATC 812
Db 1236 TCTGATCCCTATATTTGGACCTTATGATCGATCGATGCAAGTGGTGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAACAGTTGATTCAGATCGGTTTCATCAATTCGAATGATTTTGTAT 872
Db 1296 AATTGAATCATTAAAGAGCTGTTGATTCGTGTTGATTCCTGCTTGAAGCGATCATAGT 1355
QY 873 AGATCGCATAGTATGCTAGCTTAAAGACTGCAAAACAGGTCGATATATTTCTTC 932
Db 1356 TGATAGGCTAGTATGATCCAGCCTTCAAGAACTTCAATAGATCCAGACATATCTTG 1415
QY 933 CAGTTGTGTAACACAAAAGAGTTGCGATCATATAGCAAAAGCTGGTATGCAATCACTT 992
Db 1416 TAGTGCATATACCAAAAGAGTTGTTGATCAGCTGCGAAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479

RESULT 12
PCT-US93-07347-6
Sequence 6, Application PC/TUS9307347
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07347

FILING DATE: 19930805
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-07347-6
Query Match 4.7%; Score 155.2; DB 5; Length 5890;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAATGGATGTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1176 GGTAAATGGCTGTTATCGTACTATGATAAAGTTCCTGATGGTTTTTATATGATGAATGG 1235
QY 753 GATGACCCATATGATGTCATATGACCAATCTGCAAGAGGATGGGCGTATACCATC 812
Db 1236 TCTGATCCCTATATTTGGACCTTATGATCGATCGATGCAAGTGGTGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAACAGTTGATTCAGATCGGTTTCATCAATTCGAATGATTTTGTAT 872
Db 1296 AATTGAATCATTAAAGAGCTGTTGATTCGTGTTGATTCCTGCTTGAAGCGATCATAGT 1355
QY 873 AGATCGCATAGTATGCTAGCTTAAAGACTGCAAAACAGGTCGATATATTTCTTC 932
Db 1356 TGATAGGCTAGTATGATCCAGCCTTCAAGAACTTCAATAGATCCAGACATATCTTG 1415
QY 933 CAGTTGTGTAACACAAAAGAGTTGCGATCATATAGCAAAAGCTGGTATGCAATCACTT 992
Db 1416 TAGTGCATATACCAAAAGAGTTGTTGATCAGCTGCGAAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479

RESULT 13
US-08-003-311B-4
Sequence 4, Application US/08003311B
Patent No. 544166
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 544166ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800

PRIOR APPLICATION DATA: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-003-311B-4

Query Match 4.7%; Score 155.2; DB 1; Length 6295;
Best Local Similarity 69.4%; Pred. No. 6.7e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAAATGGATGTCATATTTGGAGAAAGTCCAGATGGTTTATCTAATTCATGG 752
Db 1598 GGTAATGGCTGCTTATCGTACTATATAAGTTCTCATGGTTTATATGATGATGG 1657
QY 753 GATGAGCCCATATGTATGTCTATATGACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db 1658 TCTGGATCCCTATATTTGGACCTTATGATCGATGCAAGTGGTGCATCCCTTC 1717
QY 813 ATTGAACTCTGAAACAGTTCATCCAGATCGGTTCATCAATTTGAAGTATTTGAT 872
Db 1718 AATTGAATCATTAAGAGCTGTGATTTCTGGTGTGATTTCTCGCTTGAAGGATCATAGT 1777
QY 873 AGATCGGCATAGTGTAGTCTAGCTTAAAGAACTGCAAAACAGGGTGCATATATTTCTC 932
Db 1778 TGATAGCGGTAGTGTAGTCCAGCTTCAAGAACTTCACATAGAGTCCAGCATATCTTG 1837
QY 933 CAGTTGTGTAAACCAAAAGAGTTCCAGATCATATAGCAAGCTGGTATGCAATCACTT 992
Db 1838 TAGCTGCATTAACCAAAAGAGTTTGTATGATGCTGCAAGAGCTTATCTGCAATCGPAT 1897
QY 993 GGGG 996
Db 1898 GGGG 1901

RESULT 14
US-08-261-432-4
Sequence 4, Application US/08261432
Patent No. 560322
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kiebler, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 560322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432

FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-261-432-4

Query Match 4.7%; Score 155.2; DB 1; Length 6295;
Best Local Similarity 69.4%; Pred. No. 6.7e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAAATGGATGTCATATTTGGAGAAAGTCCAGATGGTTTATCTAATTCATGG 752
Db 1598 GGTAATGGCTGCTTATCGTACTATATAAGTTCTCATGGTTTATATGATGATGG 1657
QY 753 GATGAGCCCATATGTATGTCTATATGACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db 1658 TCTGGATCCCTATATTTGGACCTTATGATCGATGCAAGTGGTGCATCCCTTC 1717
QY 813 ATTGAACTCTGAAACAGTTCATCCAGATCGGTTCATCAATTTGAAGTATTTGAT 872
Db 1718 AATTGAATCATTAAGAGCTGTGATTTCTGGTGTGATTTCTCGCTTGAAGGATCATAGT 1777
QY 873 AGATCGGCATAGTGTAGTCTAGCTTAAAGAACTGCAAAACAGGGTGCATATATTTCTC 932
Db 1778 TGATAGCGGTAGTGTAGTCCAGCTTCAAGAACTTCACATAGAGTCCAGCATATCTTG 1837
QY 933 CAGTTGTGTAAACCAAAAGAGTTGCGATCATATAGCAAGCTGGTATGCAATCACTT 992
Db 1838 TAGCTGCATTAACCAAAAGAGTTTGTATGATGCTGCAAGAGCTTATCTGCAATCGPAT 1897
QY 993 GGGG 996
Db 1898 GGGG 1901

RESULT 15
US-08-003-311B-3
Sequence 3, Application US/08003311B
Patent No. 5444166
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kiebler, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5444166ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1

Sat Oct 25 11:01:50 2003

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6312 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-003-311B-3

Query Match 4.7%; Score 155.2; DB 1; Length 6312;
Best Local Similarity 69.4%; Pred. No. 6.7e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY	693	GGTAAATGGATGCATGTCATATTTGGAGAAAGTGCAGATGGTTTTTATCTAATTCATGG	752
Db	1598	GGTAAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGGTTTTATATGATGAATGG	1657
QY	753	GATGGACCCATATGATGGTCATATTATGACCAATCTGCAGAGGATGGGGTATACCATC	812
Db	1658	TCTGGATCCCTATATTGGACCTTATGCATCGACCTGCATGAAAGTGGTCGATCCCTTC	1717
QY	813	ATTGGAATCTCGAAACACAGTTGATTCAGCATCGGTTTCATCAATTCGAAGTAGTTTGTAT	872
Db	1718	AATTGAATCATTAAGAGCTGTTGATTCGTTGATTCCTCGCTTGAAGCGATCATAGT	1777
QY	873	AGATCGGCATAGTATGCTAGCTTAAAGAACTGCAAAACAGGGTGCATATATTTCTTC	932
Db	1778	TGATAGGCGTAGTATGCCAGCCTTCAAGGAAGTTCACAAATAGAGTCCACGACATATCTTG	1837
QY	933	CAGTTCTGTAAACACAAAGAGGTTGCAGATCATATAGCAAAAGCTGGTATGCAATCACTT	992
Db	1838	TAGCTGCATTACCACAAAGAGGTTGTTGATCGCTGCAAGCTTATCTGCAATCGTAT	1897
QY	993	GGGG 996	
Db	1898	GGGG 1901	

Search completed: October 24, 2003, 05:12:29
Job time : 200 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 04:53:49 ; Search time 837 Seconds

(without alignments)
10528.552 Million cell updates/sec

Title: US-09-904-389-1

Perfect score: 3286

Sequence: 1 attcgatttcggaagaga.....aaaaaaaaaaaaaaaa 3286

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PTCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PTCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3283	99.9	3286	10	US-09-904-389-1
2	898.8	27.4	2466	12	US-10-171-404A-47
3	412	12.5	2892	10	US-09-938-842A-1073
4	296.4	9.0	2661	10	US-09-938-842A-1085
5	270.2	8.2	2211	10	US-09-938-842A-1577
6	141.6	4.3	255	10	US-09-878-574-10192
7	136.6	4.2	397	10	US-09-878-574-46
8	136	4.1	1662	10	US-09-938-842A-1014
9	111.8	3.4	1638	10	US-09-938-842A-903
10	84.8	2.6	246	9	US-09-932-876-1947
11	84.2	2.6	1063	14	US-10-106-698-2068
12	81.6	2.5	1365	9	US-09-757-982-6
13	81.6	2.5	2120	9	US-09-757-982-4
14	74.8	2.3	463	9	US-09-770-444-370
15	72.6	2.2	2975	12	US-10-440-341-2
16	72.6	2.2	2977	10	US-09-969-347-207

17	72.6	2.2	2977	12	US-10-371-138-1	Sequence 1, Appli
18	72.6	2.2	2977	14	US-10-057-550-25	Sequence 25, Appli
19	72.6	2.2	2977	14	US-10-173-225B-64	Sequence 64, Appli
20	72.4	2.2	1428	10	US-09-938-842A-882	Sequence 882, Appl
21	72.2	2.2	2640	10	US-09-938-842A-1270	Sequence 1270, Ap
22	71.8	2.2	2505	10	US-09-947-199-3	Sequence 3, Appli
23	71.8	2.2	3025	10	US-09-947-199-1	Sequence 1, Appli
24	71.6	2.2	2229	12	US-10-440-341-6	Sequence 6, Appli
25	70.4	2.1	2288	14	US-10-205-342-2	Sequence 2, Appli
26	70	2.1	2510	14	US-10-057-550-89	Sequence 89, Appli
27	70	2.1	2510	14	US-10-173-225B-67	Sequence 67, Appli
28	69.2	2.1	816	14	US-10-101-464A-252	Sequence 252, App
29	67.8	2.1	3850	8	US-08-910-386A-19	Sequence 19, Appli
30	65.2	2.0	1839	10	US-09-938-842A-1168	Sequence 1168, Ap
31	65	2.0	2607	10	US-09-938-842A-1269	Sequence 1269, Ap
32	63.4	1.9	1065	10	US-09-938-842A-1466	Sequence 1466, Ap
33	63.2	1.9	2028	10	US-09-938-842A-65	Sequence 65, Appli
34	63	1.9	1789	10	US-09-840-704-1	Sequence 1, Appli
35	62	1.9	1607	9	US-09-925-302-336	Sequence 336, App
36	61.6	1.9	1902	13	US-10-086-464-10	Sequence 10, Appli
37	61.6	1.9	1939	13	US-10-086-464-9	Sequence 9, Appli
38	61.4	1.9	603	10	US-09-867-701-10287	Sequence 10287, A
39	60.6	1.8	2736	10	US-09-938-842A-56	Sequence 56, Appli
40	60	1.8	826	9	US-09-770-445-711	Sequence 711, App
41	59.8	1.8	1986	10	US-09-938-842A-1066	Sequence 1066, Ap
42	59.8	1.8	2719	10	US-09-917-800A-1405	Sequence 1405, Ap
43	59.6	1.8	2675	10	US-09-867-828A-1	Sequence 1, Appli
44	59.4	1.8	509	11	US-09-918-995-19612	Sequence 19612, A
45	59	1.8	667	14	US-10-101-464A-369	Sequence 369, App

ALIGNMENTS

RESULT 1

US-09-904-389-1
; Sequence 1, Application US/09904389
; Patent No. US20020129404A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Schuster, Debra K.
; TITLE OF INVENTION: CTRI HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)...(81)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (593)...(594)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-389-1

Query Match	99.9%	Score 3283;	DB 10;	Length 3286;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3286;	Conservative	0;	Mismatches	0;
			Indels	0;
Gaps	0;			
QY	1	ATTCGATTGTCGGGAGAGAGACAGAGAAATTAACCAACAGAAATCTCCACACACAAACCT	60	
Db	1	ATTCGATTGTCGGGAGAGAGAGAGAAATTAACCAACAGAAATCTCCACACACAAACCT	60	
QY	61	TCCACCCCTTCAACAATGGCGNCGAATCTAGGGTTTCTATGGGTTTAAGGTGATACAGTTT	120	
Db	61	TCCACCCCTTCAACAATGGCGNCGAATCTAGGGTTTCTATGGGTTTAAGGTGATACAGTTT	120	

QY	121	CCTAATTTCTCCATGGAAATGCGCTGGACGAGTCTGATTAATCTCTTTTAAGTCAAAAT	180	1201	AGAGATGATGCTTTCATCTTGCTTGTAGGTTGGGCTTGATAGGAATATCTCATCGAT	1260
Db	121	CCTAATTTCTCCATGGAAATGCGCTGGACGAGTCTGATTAATCTCTTTTAAGTCAAAAT	180	1201	AGAGATGATGCTTTCATCTTGCTTGTAGGTTGGGCTTGATAGGAATATCTCATCGAT	1260
QY	181	CGGACGAGGAGGTTGGAACGGGAGCTTCCACTTCTTTTACGACTCCGTAGCAGCTGGG	240	1261	CTGATTTGGGAGGCGAGTTGCTTATGCCCACCTGATCTTTTGGCTCAATGGTCCGATCACC	1320
Db	181	CGGACGAGGAGGTTGGAACGGGAGCTTCCACTTCTTTTACGACTCCGTAGCAGCTGGG	240	1261	CTGATTTGGGAGGCGAGTTGCTTATGCCCACCTGATCTTTTGGCTCAATGGTCCGATCACC	1320
QY	241	GGAAACGTTATCAAAAGGAGAACCGATAGGTTTGGATGGGATGGGATGGTATCAC	300	1321	ATCTCAATTTCTTCCACATTTGGGATTTCCAGACTTAAACCTATTGAATCTACCAATGAT	1380
Db	241	GGAAACGTTATCAAAAGGAGAACCGATAGGTTTGGATGGGATGGGATGGTATCAC	300	1321	ATCTCAATTTCTTCCACATTTGGGATTTCCAGACTTAAACCTATTGAATCTACCAATGAT	1380
QY	301	AGGTTAAACACGACGAGGCTATCGGATAGGAAACCTGATTTCAATGGATTTGGTTTACAGAGA	360	1381	TTCAAGTCTAGTGGCCCAACAGATTTTCTTGGATAGCAATCACTTAATCTTGTATTTCAT	1440
Db	301	AGGTTAAACACGACGAGGCTATCGGATAGGAAACCTGATTTCAATGGATTTGGTTTACAGAGA	360	1381	TTCAAGTCTAGTGGCCCAACAGATTTTCTTGGATAGCAATCACTTAATCTTGTATTTCAT	1440
QY	361	CATTCCAGTGAAGCAGTACGATAGTACTCTCTCTAGTGAATTTACTACGCCAGCAGC	420	1441	GAAGCTTCTTCAAGTAAATGTTGATCTGGAAGAGGATGCTGCAATCTCCGTCTATCAAAGG	1500
Db	361	CATTCCAGTGAAGCAGTACGATAGTACTCTCTCTAGTGAATTTACTACGCCAGCAGC	420	1441	GAAGCTTCTTCAAGTAAATGTTGATCTGGAAGAGGATGCTGCAATCTCCGTCTATCAAAGG	1500
QY	421	CTATCAAAACCTCGACGAAATGAGATCAATGCAATGGAAATATCTCTCGATGATGATTTTC	480	1501	CCATTAAATAGGAAGATGTAGATGGAAAAACCATAGTGGTTTACTGGTGACAGGACAGA	1560
Db	421	CTATCAAAACCTCGACGAAATGAGATCAATGCAATGGAAATATATCTCTCGATGATGATTTTC	480	1501	CCATTAAATAGGAAGATGTAGATGGAAAAACCATAGTGGTTTACTGGTGACAGGACAGA	1560
QY	481	CGAGTGATGAAGCTGTGGGAAGTGGAGTTCTGCTCGAAAGAGCTGGGCCCGACGAGC	540	1561	AATTTCTCAGTTATTAATAAAAAAGCAGCCCAACTGAATCTCAAGATGGAAAGTCTGAG	1620
Db	481	CGAGTGATGAAGCTGTGGGAAGTGGAGTTCTGCTCGAAAGAGCTGGGCCCGACGAGC	540	1561	AATTTCTCAGTTATTAATAAAAAAGCAGCCCAACTGAATCTCAAGATGGAAAGTCTGAG	1620
QY	541	GAAGAGAGCTTTCAAGTTCAGACAGCCCTTGGTTCTTAGGCTTTCTTCAGATGNNACTTGT	600	1621	CAATTTAGATCATGTGTGCTTCTCCATATAGTGTACAGTCGACCCCTTTTGTAGAAAAT	1680
Db	541	GAAGAGAGCTTTCAAGTTCAGACAGCCCTTGGTTCTTAGGCTTTCTTCAGATGNNACTTGT	600	1621	CAATTTAGATCATGTGTGCTTCTCCATATAGTGTACAGTCGACCCCTTTTGTAGAAAAT	1680
QY	601	GCCGATGATCCCAACTTTATCGATCCGATTCAGACGAGGAGCTTTAAGATCGTTATCG	660	1681	GTAGTCCCTTTAAGCCATATCTCACACATTTGGTTCTGAAAGATTCGGAGCATCTCTTAGCA	1740
Db	601	GCCGATGATCCCAACTTTATCGATCCGATTCAGACGAGGAGCTTTAAGATCGTTATCG	660	1681	GTAGTCCCTTTAAGCCATATCTCACACATTTGGTTCTGAAAGATTCGGAGCATCTCTTAGCA	1740
QY	661	ATTTGAGTGGGCGCATCTCGCATCGTTCTGGTGAATGATGATGATATTTGGAG	720	1741	TTGTCTCATCCAAAGGATGGATCATGTTAAACAATTTACCAATTTGGTTTCCATGGGACAGAT	1800
Db	661	ATTTGAGTGGGCGCATCTCGCATCGTTCTGGTGAATGATGATGATATTTGGAG	720	1741	TTGTCTCATCCAAAGGATGGATCATGTTAAACAATTTACCAATTTGGTTTCCATGGGACAGAT	1800
QY	721	AAAGTCCAGATGTTTTATCTAATCATCGGATGACCCATATGATGATGATGATG	780	1801	ATTAGAAAACCAATGAGCTTTCCCTTGGCTTAGAAGATTTGGTTATTCATGGGACAGAT	1860
Db	721	AAAGTCCAGATGTTTTATCTAATCATCGGATGACCCATATGATGATGATGATG	780	1801	ATTAGAAAACCAATGAGCTTTCCCTTGGCTTAGAAGATTTGGTTATTCATGGGACAGAT	1860
QY	781	ACCAATCTCAGAGAGTGGGCTATACCATCATTTGAATCTCTGAAACAGTTGATTC	840	1861	CTTGATTTGAGGAGGAAAATTTGGAGCAGGTTCTTTTGGGACTGTATATCGTGGTGAGTGG	1920
Db	781	ACCAATCTCAGAGAGTGGGCTATACCATCATTTGAATCTCTGAAACAGTTGATTC	840	1861	CTTGATTTGAGGAGGAAAATTTGGAGCAGGTTCTTTTGGGACTGTATATCGTGGTGAGTGG	1920
QY	841	AGCATCGGTTTCATCAATTGAAGTAGTTTGTAGATCGGCATAGTGTAGCTTAAAA	900	1921	CATGGCTCTGATGTTGCTGTGAAGTCCCTCACAGAACAGACTTCCATCTCGAAGCTGTT	1980
Db	841	AGCATCGGTTTCATCAATTGAAGTAGTTTGTAGATCGGCATAGTGTAGCTTAAAA	900	1921	CATGGCTCTGATGTTGCTGTGAAGTCCCTCACAGAACAGACTTCCATCTCGAAGCTGTT	1980
QY	901	GAACTCRAAAACAGGTCATTAATTTCTCCAGTTGTGTAAACCAAGAGAGTTGCA	960	1981	AATGAGTTTCTGAGAGAGGTTGCTATCATGAAAATCTTTTACGACATCTTAATATTGACTG	2040
Db	901	GAACTCRAAAACAGGTCATTAATTTCTCCAGTTGTGTAAACCAAGAGAGTTGCA	960	1981	AATGAGTTTCTGAGAGAGGTTGCTATCATGAAAATCTTTTACGACATCTTAATATTGACTG	2040
QY	961	GATCATATAGCAAAAGCTGATGCAATCACTTGGGGGTTTCAGTTTCTGAGGGGAGAAGAT	1020	2041	TTTATGGTGGGTGACCAAGCCCAACCACTTCCATTTGTCACCCGAATATCTATCTGAGA	2100
Db	961	GATCATATAGCAAAAGCTGATGCAATCACTTGGGGGTTTCAGTTTCTGAGGGGAGAAGAT	1020	2041	TTTATGGTGGGTGACCAAGCCCAACCACTTCCATTTGTCACCCGAATATCTATCTGAGA	2100
QY	1021	GACTTGGTTTCTGCGTGAAGAAATGACCGATGACTTTAAAGGAATGTTTGGGATCTGCT	1080	2101	GATAGCTTGTATAGGCTTTTGATAGTCAAGTGTCTCAAGACATAGATGAACACGTCGA	2160
Db	1021	GACTTGGTTTCTGCGTGAAGAAATGACCGATGACTTTAAAGGAATGTTTGGGATCTGCT	1080	2101	GATAGCTTGTATAGGCTTTTGATAGTCAAGTGTCTCAAGACATAGATGAACACGTCGA	2160
QY	1081	GTGATTTCCCTTATGACGCTTATCTGTGTGGCTTTGTAGACATCGTGTCTTTTATTCAA	1140	2161	ATAAATATGGCTTTTGTATGGGCAAGGAAATGAATCTACTCTCCACAGAGCTGATCTCCA	2220
Db	1081	GTGATTTCCCTTATGACGCTTATCTGTGTGGCTTTGTAGACATCGTGTCTTTTATTCAA	1140	2161	ATAAATATGGCTTTTGTATGGGCAAGGAAATGAATCTACTCTCCACAGAGCTGATCTCCA	2220
QY	1141	GTCTAGCTGATTCATTAATGATTTACCTGTGAAATGCGAAGGATGATTAATTTGCACT	1200	2221	ATTGTTTCTATCGTGTATTTAAATCACCGAATCTGTTAGTTGCAAGAAAGTATACAGTCAAG	2280
Db	1141	GTCTAGCTGATTCATTAATGATTTACCTGTGAAATGCGAAGGATGATTAATTTGCACT	1200	2221	ATTGTTTCTATCGTGTATTTAAATCACCGAATCTGTTAGTTGCAAGAAAGTATACAGTCAAG	2280
				2281	GFTTGTGATTTTGGTCTCTCCCGTTTAAAGGACGACCATTTCTTTCATCCAAATCTGCA	2340

```

; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
; FILE REFERENCE: 16313-0119
; CURRENT APPLICATION NUMBER: US/10/171,404A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/295,680
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-171-404A-47

Query Match      27.4%; Score 898.8; DB 12; Length 2466;
Best Local Similarity 64.3%; Pred. No. 1.4e-235;
Matches 1582; Conservative 0; Mismatches 661; Indels 216; Gaps 7;

Qy 253 AAAGGGAGAACCGATAGGGGTTTTGATTGGGATGGAGTGGTATCACAGGTTAAACACG 312
Db 166 AGAGGGGGATTTGATTGGGATCCTAGCGGTGGTGGTGGTATCATAGGTTGAATAAT 225

Qy 313 CAGCGGTATCGGATAGGGAACCTGT-----ATTCAATGGATTGGTTACAGACATTC 366
Db 226 CAACCCGAATCGGGTTGGGGAATAATATGATGCTTCGTCTCTAGGGTTGCAAGGCAATCC 285

Qy 367 AGTGGAGACGAGCTACGATGATAGCTCTCTCTAGTATGATACACGACCGACGCTATCA 426
Db 286 AGTGGAGTAGTTTCGGTGAGAGCTTTTGTCTGGGATATTATCATCGCTACGCTTTC- 344

Qy 427 AACCTGCGAGCAATAGATCAATGATGGAATATATCTCGATGATGATTCGAGTTC 486
Db 345 --TSCGCGCGCTAACGAGATCGAATCTGTGTGATTTCTCAAGATGATGGGTTTAGGCTT 402

Qy 487 ATGAAAGCTGTGGGAAGTGGAGTTCG----- 513
Db 403 GGATTTGGTGGTGGAGAGATTGAGGATACAGATGGCGCGGACTCCGCTGGAGGG 462

Qy 514 -----TCTGGAAAGAGCTGGCGCGAGCAGAGAGAGAGCTTTCACTGAGAGAGCC 567
Db 463 TCTTCATCTGGGAAGAGCTGGCGCGAGCAGAGAGAGAGTATATCAGCTGAGCTTGA 522

Qy 568 TTGGTTCTTAGGCTTTCTTCAGATGNNACTTCTGCGGATGATCCCACTTTATGATCCG 627
Db 523 TTGGGTTAAGGCTTTCTGCGGAGGCTACTTGTGCGAGCATCCGAATCTTCTGATCCT 582

Qy 628 ATTCCAGACGAGCAGCTTTAAGATCGTTATCGATTTTCACTGAGGCGCATCTCGCATCG 687
Db 583 GTACCGGACGAGTCTCTTTACGGACTTCGCCAAGTTTCAAGCGGAAACCGTTTCACTCGT 642

Qy 688 TTCTGGGTAATGGATGATGATCATATTTGGAGAAAGTCCAGATGCTTTTATCTAATT 747
Db 643 TTCTGGGTTAATGGCTGCTTATCGTACTATGATGATGATGATGATGATGATGATGATG 702

Qy 748 CATGGGATGACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807
Db 703 AATGGTCTGGATCCCTATATTTGGACCTTATGACCTGATGATGATGATGATGATGATG 762

Qy 808 CCAATCTTGAATCTCTGAAACAGTGTGATTCAGCATCGGTTTCAATTCATGATGATG 867
Db 763 CCTTCAATTGAATCATTAAGAGCTGTGATTTCTGTTGTTGATTTCTGCTTGAAGCGATC 822

Qy 868 TTGATAGATCGGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 927
Db 823 ATAGTTGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882

Qy 928 TCTTCCAGTTGTGTAAACCAAGAGGTTGAGATGATGATGATGATGATGATGATGATG 987
Db 883 TCTTGTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 942

Qy 988 CACTTGGGGGTTTCACTTCTGAGGAGAGATGATGATGATGATGATGATGATGATGATG 1047
```

RESULT 2

US-10-171-404A-47

; Sequence 47, Application US/10/171404A

; Publication No. US20030177529A1

; GENERAL INFORMATION:

943 COTATGGGGGTCAGTTATCATGGGGAAGATGAGTTGGTCCCATGTGGGAAGGATGC 1002
1048 AGCGATGACTTAAAGGAATGTTGGGATCTGCTGTGATTCCTTTATGCACTTATCTGTT 1107
1003 ATTGATGCTTAAAGGAATCTTTAAA--GTGGTGGTCCCATAGTAGCCTCTCTGTT 1059
1108 GGCCTTTGTAGACATCGTCTTTTATTCAAGTCTAGCTGATTCAAATTTGATTTACCC 1167
1060 GCACCTCTGCAGACATCGAGCTTACTCTTCAAGTACTGGCTGACATATGATTTACCC 1119
1168 TGTGCAATTTGCCAAAGGATGTAATATTTGCACTAGAGATGATGCTTCATCTCCCTGTT 1227
1120 TGTGCAATTTGCCAAAGGATGTAATATTTGTAATAGAGAGATGCGCTTCTGCTCTGTC 1179
1228 AGGTTGGGCTTGATAGGAATATCTCATGATCTGATTTGGAGGCGAGGTTGCTATGC 1287
1180 AGGTTGGGCTTGATAGGAGTACCTGTTGATTTAGTAGGAAGCCAGGTCACTTAGG 1239
1288 CAACCTGATTTCTTGTCTCAATGGTCCATCCATCTCAATTTCTTCCACCATTCGCAAT 1347
1240 GAGCCTGATTTCTTGTAAATGGTCTTCACTATCTCAATTTCTTCTCTGCGGTT 1299
1348 CAAAGACTAAACCTATTGAATCTACCATGATTTAGTTCAGTCTAGTCCGCAACAGATTTTC 1407
1300 CCACGACCAAGCCAGTTGAACCCGACGTCGATTTTAGGTTACTAGCCAAACATATTTTC 1359
1408 TTGGATAGCAATCACTTAATCTTGTATTGATGAAGCTTCTTTCAGGTAAATGTTGTAAT 1467
1360 TCCGATAGCAGTCTTAACTTCTGTTTTCGATCTCGCATCAG----- 1402
1468 GGAAGGATGCTGCATTTCCGCTATCAAGGCCATTAATAGAGGATGATAGTGA 1527
1403 ----ATGATATGGATTTCTCAATTTTATAGGCAATATGATAATCCGGTGGAGAAAT 1458
1528 AAAACCATAGTGTACTGTCACAGGACAGAAATTTCTGATTTATAATAAAAAAGCA 1587
1459 GAGCATTGGCAAAATGGTG----- 1480
1588 GCCCAACTGAATCAAGATGGAAGTCTGAGCAATTTAGATCATGTTGCTTCTCCA 1647
1481 ----- 1480
1648 TATAGTGTACAGTCGACCCCTTTTGTAGAAATGTAGTCCCTTTAAGCCATATCTCAC 1707
1481 -----GTGGCTCTTTCGCCACC 1497
1708 ATTGGTTCTGAAGATTCGAGCATCTCTTAGCATGTCATCCCAAGATGATCATGTT 1767
1498 AGTGCTAATATGCTCCACAGAACATGATCGGTGCTCAATCAAAATGAAGCAGCACT 1557
1768 AACAAATTACCATTTGTCATGTTAGTGTAGTATTAGAAACCAAAATGAGCTTTCCCTT 1827
1558 ATGATGCCCAACCAATCAGTCAGCCAGTTCNAACAGGGCAATAGGAACTTGGACTT 1617
1828 GGCCTAGAAGATTTGTTATTCATGACAGATCTTTGATTTGAGGAGAAATTTGGAGCA 1887
1618 GATGGTGATGATATGGACATCCCGTGGTGTGATCTTAATATAAAGAAAGATTTGGAGCA 1677
1888 GGTCTTTGGGATGTATATCGTGTGAGTGCATGCTGTGATCTTCTGTGAAGATC 1947
1678 GGTCTTTGGGCTGTCCACCGTGTGATGTCATGCTGATGCTGATGCTGTGAAAT 1737
1948 CTCACAGAACAAAGACTTCCATCTCTGAAACGTTGTTAATGAGTTCTGAGAGAGTTGCTATC 2007
1738 CTCATGAGCAAGACTTCCATCTGAGCGTGTAAATGAGTTCTTAAGAGAGTTGCGATA 1797
2008 ATGAATCTTTACACATCTTAATATTTACTGTTTATGGTGGTGGTGAAGCCACCA 2067
1798 ATGAACGCGCTTCGCCACCTTAATTTCTTCTCATGGTGGTGGTCTCACTCACTCA 1857
2068 AACTTTGTCATTTGCCCAAGATATCTATCGAGAGGTAGCTTGTATAGGCTTTTGTATAG 2127
1858 AATTGTCAATAGTGACAGAAATTTTGTCAAGAGGTAGTTTATACAGACTTTTGTGATAAA 1917

QY 2128 TCAGGTGTCA--AAGCATAGATGAACACGCTCGAATAAATATATGCTTTTGTATGGCA 2184
DB 1918 AGTGGAGCAAGGAGCAATTAGATGAGACAGCTCGCTGAGTATGCTTATGATGTGCT 1977
QY 2185 AAGGGAATGAACCTCTCCACAGACGTGATCTCCAAATTTGTTTCATCGTGAATTAATCA 2244
DB 1978 AAGGGAATGAATATCTTCACAATCGAATCTCCAAATTTGTCATAGAGATCAAAATCT 2037
QY 2245 CCGNATGTTGTTGATGACAGAGATGATACAGTCAAGTTTGTGATTTTGGTCTCTCCGCT 2304
DB 2038 CCAAACTTATTTGTTGACAAAAAATATACATCAAGTTTGTGATTTTGGTCTCTCGGA 2097
QY 2305 TTAAAGCAGCAGCAATTTCTTTCATCCAAATTCGAGCTGGAAACACCTGAATGGATGGCA 2364
DB 2098 TTGAAGCCAGCAGCTTTCTTCTCGAAATCAGCAGCTGGAAACCCCGAGTGGATGGCA 2157
QY 2365 CCAGAGTACTACCGGATGAACCATCAATGAAGTCAAGTGTGTTTACAGCTTTGGAGTG 2424
DB 2158 CCAGAGTCTCTCGAGATGAGCCGTCTAATGAAGTCAAGTGTGATGATGTTTGGGTC 2217
QY 2425 ATTTTGGGAGTTGGCACTTTTCCAAAGCCATGTTGTAATCTAAACCCAGCTCAGTT 2484
DB 2218 ATCTTTGGGAGCTTGTCTACATTTCAACACCATGGGTAACTTAAATCCGGCTCAGTT 2277
QY 2485 GTCCAGCTGTTGATTTAAGGCAAGGCTTGACATCCACGTGATGTAATCCCAA 2544
DB 2278 GTAGTGGGTTGGTTTCAAGTGTAAAGCTGAGATCCCGGTAAATCTGATCTCTCAG 2337
QY 2545 TTGGTCTCTTAATAGTGGCTTGTCTGGCCGATGAGCCATGGAACGCTCTTTTCTTTC 2604
DB 2338 GTTGACGCAATTAATCGAGGTTTGTGGACCAATGAGCAGGATGGAAGGCTCATTTGCA 2397
QY 2605 AGCATTTGAAACCTTGAACCAATGACTTAACAGGCGCCACTCAACAAAGTCCGACA 2664
DB 2398 ACTAATAGGACTTCTGAAGCAATTCATCAATCAGCGTTCTTCGCCAACCCCTCG 2457
QY 2665 GA 2666
DB 2458 GA 2459

RESULT 3
US-09-938-842A-1073
; Sequence 1073, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1073
; LENGTH: 2892
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1073

Query Match 12.5%; Score 412; DB 10; Length 2892;
Best Local Similarity 53.2%; Pred. No. 7,5e-102;
Matches 1069; Conservative 0; Mismatches 855; Indels 84; Gaps 6;

QY 668 CTGAGGCCATCTCGCATCGGTTCTCGGTAAATGGAGTCATCTCATATTGGAGAAAGTCG 727
Db 833 CAGAATCTATCTCTACCGCTTTTCGGTAAGTGGTTGTTTATCATACAGTCACAAATAT 892
QY 728 CAGATGGTTTTATCTAAATTCATGGATGGACCCATATGATGTCATATGTCACCAATC 787
Db 893 CAGATGGATTTACAGTATATTAGAAATGGATCCGATCTCTTTGGTTGATGTGTAACAATT 952
QY 788 TGCAGAGAGATGGCGGTATACCATCATTTTGAATCTCTGAAACAGTGTGATTCAGAGATCG 847
Db 953 CTGAGGATGGCAACGAATTCATCTCTTTGTTACTCAAGGAGACTGAGCC---GAATG 1009
QY 848 GTTCATCAATTCGAAGTAGTTTGTATAGATCGGCATAGTGTAGCTTAAAGAACTGC 907
Db 1010 ATACATCAATGGAGTGGTTTTGATAGATAGACGTGAGACTCAGCTCTTAAAGAACTGG 1069
QY 908 AAAACAGGATGCATATAATTTCTTCAGTGTGTAAACCAAAAAGAGGTTCAGATCAT 967
Db 1070 AGGATAAGGCACATGAGCTGTATTTCTTCAGACAAACATGTTAGTGTCTCGAGAAAC 1129
QY 968 TAGCAAGCTGGTATGCATCATCTTTGGGGGTTTCAGTTTCTGAGGAGAAAGTACACTGG 1027
Db 1130 TTGGCAGACTTGTGGCGTCTATATAGGGGGGAATTTCCAGTGGAGCAAGGTATCTCC 1189
QY 1028 TTTCTGCCTGGAGGAATCAGCGATGACTTAAAGGAATGTTTGGGATCTCTCTGATTC 1087
Db 1190 AGAAACGATGGAAACTGGTCAGCAATAGACTCAAGGAATTTCCGGAATGTATCATTTCTC 1249
QY 1088 CTTATGACGCTTATCTGTGGCTTTGAGACATCGTCTCTTTTATTCAGATCCCTAG 1147
Db 1250 CTATAGTGTCTAAACAATGGGGCTTTGCGGCATCGTCCATCTATTTAAGAAATGG 1309
QY 1148 CTGATTCATTTGATTTACCTCTGCAATTTGCCAAAGGATGTAATATTGCACTAGAGATG 1207
Db 1310 CTGATACATAGTTTACCATGTGCGATAGCTCGAGTTGCGAGTACTGTAAAGAGACC 1369
QY 1208 ATGCTTCATCTGCCCTTTAGTTCG-----GGCTTGATAGGAATATCTCA 1255
Db 1370 ACCAATCTCTTCCCTTGTCAAGATTTGAGCATGACAGGAAGCTTTCAAGGGAATATGTAG 1429
QY 1256 TCGATCTGATTTGGAGGCCAGGTTGCTTATGCCAACCTGATTTTGTCTCAATGTCAT 1315
Db 1430 TTGACCTCATCGGGGAACCGAGGAATGTCCATGATCCGATTCCTCTATCAAGGTGAA 1489
QY 1316 CATCCATCTCAATTTCTTCACCATTCGATTTCCAGACTAAACCTATGATGATCTACCA 1375
Db 1490 CACAGTCTCAGATCTCTACCTCTTCAATAGATCATCTTACAGATTTTCCAG----- 1544
QY 1376 TTGATTTCAGGTCACTGGCCAAACAGTATTTCTTGGATAGCCCAATCACTTAATCTTGAT 1435
Db 1545 -----GCCTTGCTGATAGTACATCTCCTTGTCAAGCTG 1579
QY 1436 TTGATGAAGCTTCTTCAGGTAATGTTGTATCTGGGAAGGATCTGCATTTCTCCGTTATC 1495
Db 1580 TAGAGTCAAGAGCTTACGCACTCTTCTGAAAAACATTCAAGTTTCAGGGAGTCAAGGCC 1639
QY 1496 AAAGGCCATTAATAGGAAGGTAGATGAAAGAAACCATGCTGTTACTGTGTCAGAG 1555
Db 1640 AAGTACAAAGAAATTTGATGTCCTGATTAACCGAGGACAGTATGTTGTCTCATATTG 1699
QY 1556 ACAGAAATTTCTCAGTTATTAATAAAGAGCAGCCCACTGAATATCTCAAGATGGAAAGT 1615
Db 1700 ATCAAACTTGTGTGCAAAAGTATCATCAATGTTTTCAGAAATCTGTTCTTCAGCTC 1759
QY 1616 CTGAGCAATTTAGATCATGTTGCTTCTCTCCATATAGTGTACAGTCGACCCCTTTGTAG 1675
Db 1760 TACCACCTTGATATACCAAACTTTAGTGAAGAAAGATTTGCCCAAGAAACCTGCAAG 1819
QY 1676 AAAATGTAGTCCCTTTAAGCCATATCTCACACATTTGCTTGAAGATTCGGAGCATCTCT 1735
Db 1820 AAGAAACCGTCTTATTAAGAGATCCACACCTATGAGCAGCAAACTTATCAGTTGAC 1879
QY 1736 TAGCATGTCTCATCCCAAGGATGATCATGTTAAACAATTTACATTTGTTCTGATGTC 1795

Db 1880 CAGAGATAGTAGGCTGACACTCGAAAGATATAAAGAGAGGTTACCTGTTGACGCCA 1939
QY 1796 AGTTGATTAGAAAAACCAATGAGGCTTTCCCTTGGCTTAGAAGATTTGGTTATTTCCATGGA 1855
Db 1940 TCTCACCTTACTTGACTATTGAACCTTCTTTGGCATCAGATTGGCTGGAGGTCTCATGGA 1999
QY 1856 CAGATCTTTGATTTGAGGGAGAAATTTGAGCAGGTTCTTTTGGGACTGTATATCTGGTG 1915
Db 2000 ATGAATACATATCAAGAGCGTGTGGTGTGATCAITTTGGAACCTGTTTCATCTGCTG 2059
QY 1916 AGTGCACTGGCTCTGATGTTGCTGTGAAGATCTTCACAGAAACAGAGCTTCATCTCTGAAC 1975
Db 2060 AGTGCACTGATCAGATGTTGCTGTCAAGATTTTGTCTATTCAAGATTTTCCATGATGACC 2119
QY 1976 GTGTTAATGAGTTTCTGAGACA-----GGTTGCTATCATGAATCTTTAC 2020
Db 2120 AATTACAGAAATTTCTCAGAGAGGTATGTAAGACGGTTGCTATTAATGAACGTTCTC 2179
QY 2021 GACATCTTAATATTGTTACTGTTTATGGGTGCGGTGACCAAGCCACCAAACTTTGTCCATTG 2080
Db 2180 GTCAACCCAAATGTTGTTCTCTCTCATGGGTGCTGTGACAGAGCGACCCCGGTATCAATAA 2239
QY 2081 TCACCGAATATCTATCGAGAGGTAGCTGTATAGGCTTTTGCATAAGTCAAG---GTGTCA 2137
Db 2240 TAAACAGAAATATTGCAAGAGGCACTCTTTTCGCCCTTATCCATAGGCCAGCTTCTGGGG 2299
QY 2138 AAGACATAGATGAAACACGTCGAATAATATGCTTTTGTGATGTG----- 2181
Db 2300 AGTTGCTAGATCAGAGGAGGAGGCTACGTATGGCATTTGGATGTTGTGCTATTCCCC 2359
QY 2182 -----GCAAGGGAATGAACCTACCTCCACAGACGTGATCTCCAAITTTGTCATGCTGATT 2236
Db 2360 ATTATGCCAAGGGGCTCAACTACCTACACTGTCTTAATCTCTCTGTAGTCAITGGGACC 2419
QY 2237 TAAATACCCGAATCTGTTAGTTGACAAAGATATACAGTCAAGGTTTGTGATTTTGGTC 2296
Db 2420 TGAATCTCCAAATCTACTGTTGATAGAACTGGAAGTGAAGTTTGGATTTGGAC 2479
QY 2297 TCTCCGTTTAAAGCACGCACTTTCTTTCATCCAAATCTGCAAGCTGGAACACCTGAAT 2356
Db 2480 TTTCAAGATTTCAAGGCAAAACACTTTTCAACCATCAAAATCTGTTGCAGGAACACCTGAGT 2539
QY 2357 GATGGCACCAAGTACTAGCGATGAAACCATCAATGAAAGTCAAGATGTTTACAGCT 2416
Db 2540 GATGGCTCCAGAGTTCTTATAGGGGAAACCGAACAAACGAGAAATCAGATGTTTACAGTT 2599
QY 2417 TTGGAGTGTATTTTGGGAGTTGGCAACTTTTGCAACAGCCCATGGTGTAACTTAAACCCAG 2476
Db 2600 TCGGAGTACTCTTATGGGAGTTGATTACTTTTGGCAACAGCCCTTGGAAATGGAATCAGTCTG 2659
QY 2477 CTCAGGTTGTCAGCTGTGTAATTAAGGCAAAAGGCTTGAATCCAGGTGATGTAA 2536
Db 2660 CTCAGGTTGTCAGGAGTTCGATTTCCAGAAACAGGCGGCTTATAATTCCTCCCAACACT 2719
QY 2537 ATCCCAAAATTTGCTTCTTAATAGTGGCTTCTGGGCGGATGAGCCATGGAAGAGTCTCTT 2596
Db 2720 CTCCGTTTGGTATCTCTAATGGAAGCTTGTGGGCAAGATGAGCCGCTCTCAGCGGCCAG 2779
QY 2597 CTTTTCAGCAATTAATGMAACCTTGAA 2624
Db 2780 CATTTGTTAGTATAGTGGACACATTGAA 2807

RESULT 4

US-09-938-842A-1085
; Sequence 1085, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

QY 2446 TTGCAACAGCCATGGTGTATCTAACCAGCCTCAGTTGTCGAGCTGTGGATTAAAG 2505
Db 1984 ACCTTAGTACCATGGGACCGTTTGAACCTCTATTCAGGTTGTGGAGTTGTGGTTTCATG 2043
QY 2506 GGCAGAAAGGCTTACATCCACGATGATGATAATCCAAATTCCTTAAATAGTGGCT 2565
Db 2044 GATCGACGATTAGACTTACCTGAGGATTAATCCCGGATCGCATCCATATACAGGAT 2103
QY 2566 TGCTGGCCGATGAGCAGTGGAAACCTCTCTTTT 2600
Db 2104 TGTGGCAAACTGATCCAGCAAAACGACCGCTT 2138

RESULT 6
US-09-878-574-10192
; Sequence 10192, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 10192
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701103404H1
US-09-878-574-10192

Query Match 4.3%; Score 141.6; DB 10; Length 255;
Best Local Similarity 75.4%; Pred. No. 2.7e-28; Indels 3; Gaps 1;
Matches 190; Conservative 0; Mismatches 59

QY 1971 TGAACGTTGTAATGAGTTTCTGAGAGAGGTTGCTATCATGAAATCTTTACGACATCTTAA 2030
Db 3 TGAACGTTCTAGGAATTCCTGAGGAGGTTTGAATATGAAGGCTTACGGCATCCAAA 62
QY 2031 TATTGTACTGTTATGGTGGCTGACCAAGCAGCAAACTTGTCTATGTCACCAATA 2090
Db 63 CATTTGTTTACTTATGGTGCAGTCACTAGAGCTCTCTAATTTATCAATTTGTACCGAATA 122
QY 2091 TCTATCGAGAGTAGCTTGTATAGGCTTTTGCATAAGTCAGGTGTCAAAGACA---TAGA 2147
Db 123 TTTGTCAGGGTAGCTTTGTACAGGCTTTGCATAAACCTGGCGCTACAGAGATGTTGA 182
QY 2148 TGAACACGTCGAATAAATATGGCTTTTGTATGGCAAGGGAATGAATACCTCCACAG 2207
Db 183 TGAGAGACGTAGGCTTATGATGCTGATGATGTTGGTAAAGGAATGAATATCTTCATAA 242
QY 2208 ACGTGATCCCTCC 2219
Db 243 ACGCAATCCCTCC 254

RESULT 7
US-09-878-574-46
; Sequence 46, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574

; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 46
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-G1
US-09-878-574-46

Query Match 4.2%; Score 136.6; DB 10; Length 397;
Best Local Similarity 78.7%; Pred. No. 8.7e-27;
Matches 163; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1256 TCGATCTGATTTGGGAGGCCAGTTGCTTATGCCAACCTGATTCTTGTCTCAATGGTCCAT 1315
Db 2 TTGATTTAATTTGAAAGCCAGGAACCTTATCCGAGCCCTGATTCCTTCTCAATGGTCCAT 61
QY 1316 CATCCATCTCAATTTCTTCCACATTTGGATTTCCAAAGACTAAACCTTATTTGAATCTACCA 1375
Db 62 CTTCCATCTCAATTTCTTCCACCTTGGCTTTCCACGACTTAAACAGCTGAAACTACCA 121
QY 1376 TTGATTTCAAGTCACTGGCCAAACAGATTTCTTGGATAGCCATCACTTAATCTGTAT 1435
Db 122 TTGATTTCAAGTCACTGGCCAAACAGATTTCTTGGACTGTGTCTCTTGGACTTGTCT 181
QY 1436 TTGATGAAGCTTCTTCCAGGTAATGTTG 1462
Db 182 TTGACACAAATTTCTGCAGACAGTTTG 208

RESULT 8
US-09-938-842A-1014
; Sequence 1014, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1014
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1014

Query Match 4.1%; Score 136; DB 10; Length 1662;
Best Local Similarity 50.7%; Pred. No. 3.3e-26;
Matches 409; Conservative 0; Mismatches 385; Indels 12; Gaps 3;

QY 1827 TGGCTTAGAAGATTTGGTTATTTCATTCGACAGATCTTGATTTGAGGGAGAAAATTTGGAGC 1886
Db 789 TGGAACTGATGATGGAAATTTGACATGAAGCAGCTCAAAATTTGAAAAGGTTGGCATG 848
QY 1887 AGGTTCTTTTGGAGCTGATATATCGTGGTGGAGTGGCATGCTCTGATGTTGCTGTGAGAT 1946
Db 849 TGGATCATACGGGAACTATTTAGAGGAACCTTATGTTAGTCAGGAAGTAGCTATCAAAAT 908
QY 1947 CCTCACAGAACAGACTTCCATCCCTGAACGTTTAATGAGTTTCTGAGAGAGGTTGCTAT 2006

909	DB	TCTCAAGCCTGAGCGGTAAATGCGGAATGTCACAGAGTTTCTCAGGAAGTATATAT	968
2007	QY	CATGAATCTTTACGACATCCTAATATTCTACTGTTTATGGTGGCGGTACCAAGCCACC	2066
969	DB	AATGAGGAAAGTTCGGCATAAAAATGTGTCCAGTTTCATGTGTGCATGTACACGATCACC	1028
2067	QY	AAACTTGTCCATTGTCAACGAATATCTATCGAGAGGTAGCTTGATAGGCTTTTGCATAA	2126
1029	DB	AAACCTCTGCATTGTGCACAGTTCAAGACTCGGGGAGCATTTAATGATTTCTTCCAA	1088
2127	QY	GTCAAGTGTCAAAGACATAGATGAACAACGTGCAATAAATATGGCTTTTGATGTGGCAAA	2186
1089	DB	ACACAAAGGGGTTTTAAAAATTCAATC---TTTGCTCAAAGTGGCACTCGACGTCTCGAA	1145
2187	QY	GGGAATGAACACTCTCACACAGCGTGATCCTCCAATTGTTTCATCTGTGATTTAAAAATCACC	2246
1146	DB	AGGAATGAATTATCTGCATCAAAACAAT-----ATTATTATAGAGACCTTAAAGCTGC	1199
2247	QY	GAACTGTGTAGTTCACACAGAGTATACAGTCAAGTTTGTGATTTTGGTCTCTCCGTTT	2306
1200	DB	TAATCTTCTTATGACCAACATGAAGTTGTCAAAGTTGCCGATTTTGGTGTGGCAGGT	1359
2307	QY	AAAGCACGCGCATTTCTTTTCACAAATCTGCAGCTGGAAACCTCGAATGGATGGCACC	2366
1260	DB	GCAGACTCAGTCAGGGTT---ATGCAGCGGAAACAGGGACATACCGATGGATGGCTCC	1316
2367	QY	AGAACTACTACGGCATGAACCATCAAAATGAABAGTCAGATGTTTACAGCTTTGGAGTGT	2426
1317	DB	AGAGTCAITGAGCACAAACCTTATGATCACAGGCGAGATGTTCTCAGCTACGGATGT	1376
2427	QY	TTTGTGGAGTTGGCACTTTTGCAACGCCATGGTGTAAATCTAAACCCAGCTCAGGTGT	2486
1377	DB	GGTGTGGGAACTTTGTACTGGGAACCTCCATATCTTACTTGACTCCACTGCAAGTGC	1436
2487	QY	CGCACTGTGGATTTAAGGCAAAAGCGTTGACATCCCAACGTGTAAATCCCAATT	2546
1437	DB	TGTTGGCGTTGTCCAAAGGGACCTAGAACCAAAATTCCAAAGGAAACACACCCAAACT	1496
2547	QY	GGCTTCCTTAATAGTGGCTTGTGGCCGATGAGCATGGAACGCTCTCTTTTCCAG	2606
1497	DB	GACTGAACTCTTGAGAAATGCTGGCAGCAAGACCCAGCTCTAAGACCCAAATTTTGAGA	1556
2607	QY	CATTATGAAACCTTGAACCAATGA	2632
1557	DB	AATCATAGAATGCTTAACCAACTAA	1582

RESULT 9

```

US-09-938-842A-903
/ Sequence 903, Application US/099388942A
/ Patent No. US20030160378A1
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Kreps, Joel
/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED C
/ TITLE OF INVENTION: GAME, AND METHODS
/ FILE REFERENCE: SCRIPI300-3
/ CURRENT APPLICATION NUMBER: US/09/938
/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/227,80
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: US 60/264,6
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/300,1
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 903
/ LENGTH: 1638
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-938-842A-903

```

Query Match	3.4%	Score 111.8	DB 10	Length 1638
Best Local Similarity	54.3%	Prod. No. 1.4e-19		
Matches 296	Conservative 0	Mismatches 237	Indels 12	Gaps 3
QY	1906	TATCGTGTGAGTGGCATGCTCTGATGTGTGCTGTGAAGATCCCTCAGAACCAAGACTTC	1965	
Db	877	TATAAAGTACATACTGTAGCCAGGAAGTTGCTATCAAAGTCTTAAAGCCAGAGCGTCTA	936	
QY	1966	CATCCTGAACTGTATTATGAGTTCTTGACAGAGGTTGCTATCATGAATCTTTACGACAT	2025	
Db	937	GACTCAGATCTAGAGAAGAAGTTTGCCCAAGAAGTCTTTATTATGAGGAAGTTAGACAC	936	
QY	2036	CCTAATATTGACTGTTTATGSGTGGCGTGACCAAGCCACCAAACTTGTCCATTGTCAAC	2085	
Db	997	AAAAATGTGTTCAAGTTCAATGGTGCTTGCCACCAAGCCCTCCACATCTGTATCGTTACA	1056	
QY	2086	GAATATCTATCGAGAGTACGTTGATAGCTTTTGGCATATAGTCAGGTGTCAAAGACATA	2145	
Db	1057	GAATCATGCCCCGTGGAAGTGTATATGACTATCTACACAGCAAAAGGCG--GTCTTT	1113	
QY	2146	GATGAACACGTCGAATPAATATGGCTTTTGATGGCAAGGGAATGAATCTCTCCAC	2205	
Db	1114	AAAGCTTCCAACTTTGTTTAAAGTAGCTATAGATATTTGCCAAGGGATCAGCTACTTACAC	1173	
QY	2206	AGAGCTGATCTCCCAATTGTTTCATCGTGATTTAAATATCACCGAATCTGTAGTTGACAAG	2365	
Db	1174	CAAAATAA-----CATAAATCACAGATTTGMAAGGCTGCCACCTCTTAATGACGAA	1227	
QY	2266	AAGTATACAGTCAAGGTTTGATTTTGGTCTCTCCGGTTTAAAGGCACGCAATTTCTT	2325	
Db	1228	AATGAGTGTGTTAAGGTTGCAGACTTTGGGGTGGCTAGAGTGAAGCAACAACCTGGAGTT	1387	
QY	2326	TCATCCAAATCTGCAGCTGGAAACACCTGAATGATGGATGGCACCAAGTAGTACTACGGGATGAA	2385	
Db	1288	---ATGACAGCTGAAACTGGAAACATATCCGTGGATGGCTCCAGAGGTGATAGAACACAAG	1344	
QY	2386	CCATCAATGAAGATCAGATGTTTACAGCTTTGGAGTGAITTTTGGAGGTGGCACT	2445	
Db	1345	CCATATGATCAAGGCTGACGTAITTCAGTACGGGATTTGCTATGGGAGTTGTTGACT	1404	
QY	2446	TTGCA	2450	
Db	1405	GGGAA	1409	

RESULT 10

```

RESOLV 10
US-09-923-876-1947
; Sequence 1947, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Ialagudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 05/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 1947
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700159794H1
US-09-923-876-1947

```


Db	393	CAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGGAGTACTGAAGATCTGTGA	452
Qy	2289	TTTTGGTCTCTCCCGTTTAAAGGCGCAGCATATTTCTTTTCATCAAAATCTGCAGCTGGAAC	2348
Db	453	CTTTGGTGCCTCTGGTTTCCATTAACATACA-----ACACATGCTCTTGTTTGAAC	506
Qy	2349	ACCTGAATGGATGGCACGACAGAGTACTACGCGATGAACCATCAAAATGAAAAAGTCAGATGT	2408
Db	507	TTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTCAGAAACTTGTGACAC	566
Qy	2409	TTACAGCTTTGGAGTGAATTTTGGGAGTTGGCAACTTTTGCAACGCCATGGTGTAATCT	2468
Db	567	ATATTCTTATGGTGTGGTTCTCTGGAGATGCTAAACAAGGGAGTCCCTCTTTAAAGGTTT	626
Qy	2469	AAACCCAGCTCAGGTTGTCGACGCTGTTTGAATTTAAGGGCACAAGGCTTGCATCCCAAG	2528
Db	627	GGAAGGATTACAAGTAGCTGGCTTTGTAGTGGAAAAAAACGAGAGATTAAACATTCCAAAG	686
Qy	2529	TGATGTAAATCCCAATTTGGCTTCCTTAAATAGTGGCTTCTGGGCGGATGAGCCATGGAA	2588
Db	687	CAGTTGCCCCAGAAGTTTTCCTGAACTGTTACATCAGTGTTCGGAACTGATGCCAAGAA	746
Qy	2589	ACGTCTCTCTTTTCCAGCATTTATGGAACCTTTGAAACCAATGACTTAAACAAGGCCACC	2648
Db	747	ACGGCCATCATTCAGCAAAATCATTTTCAATCTGGAGTCCATGTCAATGTACACAGGCTT	806
Qy	2649	TC 2650	
Db	807	TC 808	

```

RESULT 13
US-09-757-982-4
; Sequence 4, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPX-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)..(1411)
US-09-757-982-4

Query Match          2.5%; Score 81.6; DB 9; Length 2120;
Best Local Similarity 47.4%; Pred No. 3.4e-11;
Matches 314; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

QY 1992 GAGAGAGGTTGTCATCATGAAATCTTTACGACATCTCTAAATATGTGACTGTTTATGGGTGC 2051
Db 199 GAAAGAGGGCAGAAATACCTCAGTGTCTCTCAGTCA CAGAAACATCATCCAGTTTATGTGAGT 258
QY 2052 GGTGACCAAGCCACCACAACTTGTCNTTGTCCCGATATCTATGAGAGGTAGCTTGTA 2111
Db 259 AATCTTTGAACCTCCCAACTATGGCATTTGTCACAGAAATATGCTTCTCGGATCACTCTA 318
QY 2112 TAGGCTTTTGCATAAGTCAGCTGTGTCAAAGACATAGATGAAACACGTCGCAATAAATATGCG 2171
Db 319 TGATTACATATACAGCTTACAGAAAGTGAGGATGATATGATCACTATGACCTGGGC 378
QY 2172 TTTTGTATGTGGGAAGGGGAATGAACCTACTCTCCACAGACGCTGATTCCTCCAAATTG---TTCA 2228

```

Db	379	CACTCATGTACGCAAGGAATGCAATTATTTACATATGAGGGCTCTCTGTCAGAGTGATTCA	2388
Qy	2229	TCGTGATTTTAAATCAACCGAATCTGTGTAGTTGACAAAGAGTATACAGTCAAGTGTGTGTGA	2408
Db	439	CAGAGACCTCAAGTCAAGAAACCGTTGTTATAGCTGTGATGGAGTACTGAAAGATCTGTGA	498
Qy	2289	TTTTGGTCTCTCCCGTTTAAAGGACGCGACATTTCTTCATCCAAATCTGCAGCTGGAAC	2348
Db	499	CTTTGGTGCCTCTCGGTTCCATAACCATACA-----ACACACATGTCCTTTGGTGGAAAC	552
Qy	2349	ACTGGAATGGATGGCACACAGAGTACTACCGATGAAACCATCAATGAAAGTCAAGTGT	2408
Db	553	TTTCCCATGGATGGCTCCAGAGTTATCCAGAGTCTCCCTGTGTGAGAACTGTGTGACAC	612
Qy	2409	TTACAGCTTTGGAGTGAATTTTGTGGAGTTGGCAACTTTTGCAACAGCCATGGTGTAAATCT	2468
Db	613	ATATTCCTTATGGTGTGGTCTCTGGGAGATGCTAACAGGGAGGTCCCTTTTAAAGGTTT	672
Qy	2469	AAACCCAGCTCAGGTTGTGCGAGCTGTGTGATTTAAGGCAAAAGGCTTGACATCCCAAG	2528
Db	673	GGAAGATTTACAAGTAGCTTGGCTGTGTAGTGGAAAAAACAAGAGATTAACCATTTCCAA	732
Qy	2529	TGATGTAAATCCCAAAATGGCTTCCTTAATAGTGGCTTCTCTGGGCGGATGAGCCATGGAA	2588
Db	733	CAGTTGCCCCAGAGTTTGTCTGAACTGTTTACATCATGCTTGGGAAGCTGATGCGCAAGAA	792
Qy	2589	AGTCTCTCTTTTCCAGCATTTAGAACCTTGAAACCAATGACTAAACAAGCGCCACC	2648
Db	793	AGCGGCATCATTCAGCAAAATCATTTCAATCTGGAGTCCATGTCAAATGACACAGCCT	852
Qy	2649	TC 2650	
Db	853	TC 854	

RESULT 14
US-09-770-444-370/c
; Sequence 370, Application US/097770444
; Patent No. US20020023280A1
GENERAL INFORMATION:
; APPLICANT: Gorchach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Sladker, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 370
LENGTH: 463
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:

NAME/KEY: misc feature
 LOCATION: (1)...(463)
 OTHER INFORMATION: n = A,T,C or G
 US-09-770-444-370

Query Match 2.3%; Score 74.8; DB 9; Length 463;
 Best Local Similarity 57.8%; Pred. NO. 9.1e-10;
 Matches 133; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
 QY 2296 CTCTCCCTTTAAAGGCGACGACATCTTTTCATCCAAATCTGCAGCTGGAAACACCTGAA 2355
 Db 463 CTGTCGAGAAATATGACAGGACACAAATGAGACACAGCTCTGCAGGAATCCAGAG 404
 QY 2356 TGGATGGCACGAGAGTACTAGCGGATGAAACCATCAATGAAAGTCAGATGTTTACAGC 2415
 Db 403 TGGATGGCTCTGCACTTATCCGAATGAGCCCTTCTCGAAGAAAGTGTGATATCTTCAGT 344
 QY 2416 TTTGAGGTGATTTTGGGAGTTGGCAACTTTGCAACAGCCATGTTGTAATCTTAAACCCA 2475
 Db 343 TTAGTGTATTAATGTTGGAGCTATGCACTTAAACCCAGACCTTGGGAAGGAGTACCGCCT 284
 QY 2476 GCTCAGGTGCGGAGCTGTTGGATTTAAGGGCAAAAGGCTTGACATCCC 2525
 Db 283 GAACGGTGTATTGCTATTGCTTACGAGGAGCTCGGCTTGAGATTCC 234

RESULT 15

US-10-440-341-2
 Sequence 2, Application US/10440341
 Publication NO. US20030181413A1
 GENERAL INFORMATION:

APPLICANT: RAPP, ULF

APPLICANT: SCORM, STEPHEN M.

TITLE OF INVENTION: RAP PROTEIN KINASE THERAPEUTICS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: 1100 NEW YORK AVE., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/10/440,341

APPLICATION NUMBER: US/10/440,341

FILING DATE: 15-May-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/748,931

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: SCOTT, WATSON T.

REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: 5683/82731

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3067

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2975 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (Genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-440-341-2

Query Match 2.2%; Score 72.6; DB 12; Length 2975;
 Best Local Similarity 53.4%; Pred. NO. 1.3e-08;
 Matches 325; Conservative 0; Mismatches 254; Indels 30; Gaps 7;

QY 1879 ATTGGAGCAGGTTCTTTTGGGACTGTATATCTGGTGTAGTGGCTGCTGATGTTGCT 1938
 Db 1190 ATTGGGTGAGGCTCTTTTGGAACTGTTTAAAGGTAAATGACACGG---AGATGTTGCA 1246
 QY 1939 GTGAAGATCTCCACAGAAACAGACTTCCATCTCTGAACGTTGTTAAATGAGTTTCTTGAGAG 1998
 Db 1247 GTAAGATCTCCAAAGGTTGTGCAACCCCAACCCAGAGCAATTCAGGCCCTTCAGGAATGAG 1306
 QY 1999 GTTGCTATCATGAAATCTTTTACGACATCTTAATATTGTACTGTTTATGGGTGGGTGACC 2058
 Db 1307 GTGCTGTTCTGGCAAAACACCGCATGTGAACATTTCTGCTTTTTCATGGGGTACATGACA 1366
 QY 2059 AAGCCACCAACTGTGTCATTTGTACCGAATATCTATCGAGAGGTAGCTTTGTATAGGCTT 2118
 Db 1367 AAG--GACAACTGGCAATTTGTGCCAGTGTGCGAGGCGAGCAGCCTCTACAACAC 1423
 QY 2119 TTGCATTAAGTCAGGTGTCAAGACATAGATGAACACGTCGATTAATATGCTTTTGTAT 2178
 Db 1424 CTGCAT--GTCCAGGAGACCAAGTTTCAGATGTTCCA--GCTAATTGACATTCGCCGGCAG 1480
 QY 2179 GTGCCAAAGGGAATGAACACTACCTCCACAGACGTGATCTCTCAATTGTTTTCATCGTGAATTA 2238
 Db 1481 ACGGCTCAGGGAATGGACTATTTTGCA-----TGCAAGAACATCATCCATAGACATG 1534
 QY 2239 AATCACCAGATCTGTTAGTTGACAAGATATACAGTCAAGGTTTGTGATTTTGTGCTC 2298
 Db 1535 AATCCCAACAAATATATTTCTCCATGAAGGCTTAACAGTGAATAATTGGAGATTTTGGTTG 1594
 QY 2299 TCCGTTTAAAGGCACGACATTTTTCATCCAAATCTG-----CAGCTGGAACACCT 2352
 Db 1595 GCAACAGTAAAGTCACGCTGGAGTGTCTCAGCAGGTTGAACACACTACTGGCTCTGTC 1654
 QY 2353 GAATGGATGGCACCAAGAACTACTAG-----CGATGAACCATCAATGAAAGTCA 2403
 Db 1655 CTCTGGATGGCCCCCAGAGGTGATCCGAATGCAGGATAACACCCATTCAGTTTCCAGTCG 1714
 QY 2404 GATGTTTACAGCTTTGGAGTGATTTTGTGGGAGTTGGCAACTTTTGCAACAGCCATGCTGT 2463
 Db 1715 GATGCTACTCTATATGGCATCGTATTGTATGAATGATGACGGGGGAGCTTCCTTATTCT 1774
 QY 2464 AATCTAAAC 2472
 Db 1775 CACATCAAC 1783

Search completed: October 24, 2003, 08:16:51

Job time : 844 secs